

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 SALLRSIPA 49
Db 1 SALLRSIPA 9

RESULT 2

US-09-187-330-5
Sequence 5, Application US/09187330
Patent No. 6613740
GENERAL INFORMATION:
APPLICANT: Gozes, Ilana
APPLICANT: Brenneman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamoshtano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
FILE REFERENCE: 015280-291200US
CURRENT FILING DATE: 1998-11-06
EARLIER FILING DATE: 1997-02-07
EARLIER APPLICATION NUMBER: US 60/037,404
EARLIER FILING DATE: 1997-02-07
EARLIER APPLICATION NUMBER: WO PCT/US98/02485
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF-9 active
US-09-187-330-5

Query Match 33.3%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
Db 1 SALLRSIPA 9

RESULT 3

US-09-187-330-36
Sequence 36, Application US/09187330
Patent No. 6613740
GENERAL INFORMATION:
APPLICANT: Gozes, Ilana
APPLICANT: Brenneman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamoshtano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
FILE REFERENCE: 015280-291200US
CURRENT FILING DATE: 1998-11-06
EARLIER FILING DATE: 1997-02-07
EARLIER APPLICATION NUMBER: US 60/037,404
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF-9 active
OTHER INFORMATION: peptide adsorbed onto bovine serum albumin (BSA)
OTHER INFORMATION: as antigen
US-09-187-330-36

Query Match 33.3%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
Db 1 SALLRSIPA 9

RESULT 4

US-08-324-297A-3
Sequence 3, Application US/08324297A
Patent No. 6174862
GENERAL INFORMATION:
APPLICANT: Brenneman, Douglas E.
APPLICANT: Gozes, Ilana
TITLE OF INVENTION: Neutrotrophic Peptides of Activity
TITLE OF INVENTION: Dependent Neutrotrophic Factor
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,297A
FILING DATE: 17-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,973
FILING DATE: 22-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,087
FILING DATE: 22-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-178-1US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-324-297A-3

Query Match 33.3%; Score 40; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
Db 2 SALLRSIPA 10

RESULT 5

US-09-187-330-22
; Sequence 22, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Iliana
; APPLICANT: Breneman, Douglas E.
; APPLICANT: Baassan, Merav
; APPLICANT: Zamoshtano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; EARLIER FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: conjugated through the Cys residue to Sephadex for
; OTHER INFORMATION: affinity chromatography
US-09-187-330-22

Query Match 33.3%; Score 40; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 SALLRSIPA 49
Db 2 SALLRSIPA 10

RESULT 6
US-08-324-297A-16
; Sequence 16, Application US/08324297A
; Patent No. 6174862
; GENERAL INFORMATION:
; APPLICANT: Breneman, Douglas E.
; APPLICANT: Gozes, Iliana
; TITLE OF INVENTION: Neurotrophic Peptides of Activity
; TITLE OF INVENTION: Dependent Neurotrophic Factor
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,297A
; FILING DATE: 17-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 07/871,973
; FILING DATE: 22-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,087
; FILING DATE: 22-APR-1991
; ATTORNEY/AGENT INFORMATION:

NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-178-1US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa = an amino acid
; OTHER INFORMATION: sequence comprising from 1 to about
; OTHER INFORMATION: 40 amino acids wherein each amino
; OTHER INFORMATION: acid is independently selected from
; OTHER INFORMATION: the group consisting of naturally
; OTHER INFORMATION: occurring amino acids and mimetics"
US-08-324-297A-16

Query Match 33.3%; Score 40; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 SALLRSIPA 49
Db 2 SALLRSIPA 10

RESULT 7
US-07-871-973A-2
; Sequence 2, Application US/07871973A
; Patent No. 5767240
; GENERAL INFORMATION:
; APPLICANT: Breneman, Douglas E.
; APPLICANT: Gozes, Iliana
; TITLE OF INVENTION: Activity-Dependent Neurotrophic Factor
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/871,973A
; FILING DATE: 22-APR-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 07/688,087
; FILING DATE: 22-APR-1991
; ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330

REFERENCE/DOCKET NUMBER: 15280-178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: one-of(2, 3, 4)
OTHER INFORMATION: /product= "Xaa = unsure amino acid"
US-07-871-973A-2

Query Match 33.3%; Score 40; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
Db 5 SALLRSIPA 13

RESULT 8
US-08-324-297A-1
Sequence 1, Application US/08324297A
Patent No. 6174862
GENERAL INFORMATION:
APPLICANT: Breneman, Douglas E.
APPLICANT: Gozes, Iliana
TITLE OF INVENTION: Neurotrophic Peptides of Activity
TITLE OF INVENTION: Dependent Neurotrophic Factor
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,297A
FILING DATE: 17-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,973
FILING DATE: 22-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,087
FILING DATE: 22-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-178-1US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-324-297A-1

Query Match 33.3%; Score 40; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
Db 6 SALLRSIPA 14

RESULT 9
US-09-187-330-23
Sequence 23, Application US/09187330
Patent No. 6613740
GENERAL INFORMATION:
APPLICANT: Gozes, Iliana
APPLICANT: Breneman, Douglas E.
APPLICANT: Baassan, Merav
APPLICANT: Zamoshtano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-291200US
CURRENT APPLICATION NUMBER: US/09/187,330
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/037,404
EARLIER FILING DATE: 1997-02-07
EARLIER APPLICATION NUMBER: WO PCT/US98/02485
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: active peptide
US-09-187-330-23

Query Match 33.3%; Score 40; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
Db 6 SALLRSIPA 14

RESULT 10
US-09-187-330-21
Sequence 21, Application US/09187330
Patent No. 6613740
GENERAL INFORMATION:
APPLICANT: Gozes, Iliana
APPLICANT: Breneman, Douglas E.
APPLICANT: Baassan, Merav
APPLICANT: Zamoshtano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-291200US
CURRENT APPLICATION NUMBER: US/09/187,330
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/037,404
EARLIER FILING DATE: 1997-02-07
EARLIER APPLICATION NUMBER: WO PCT/US98/02485
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21

LENGTH: 15
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:ADNF
 OTHER INFORMATION: I/hep60-related sequence conjugated through the
 OTHER INFORMATION: Cys residue to Sephadex for affinity
 OTHER INFORMATION: chromatography
 US-09-187-330-21

Query Match 33.3%; Score 40; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 41 SALRSIPA 49
 Db 7 SALRSIPA 15

RESULT 11
 US-08-324-297A-6
 Sequence 6, Application US/08324297A
 Patent No. 6174862
 GENERAL INFORMATION:
 APPLICANT: Brennenman, Douglas E.
 APPLICANT: Gozes, Ilana
 TITLE OF INVENTION: Neurotrophic Peptides of Activity
 TITLE OF INVENTION: Dependent Neurotrophic Factor
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Crew
 STREET: One Market Plaza, Stuart Street Tower
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/324,297A
 FILING DATE: 17-OCT-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/871,973
 FILING DATE: 22-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/688,087
 FILING DATE: 22-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Garrett-Wackowski, Eugenia
 REGISTRATION NUMBER: 37,330
 REFERENCE/DOCKET NUMBER: 15280-178-1US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-324-297A-6

Query Match 33.3%; Score 40; DB 3; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.029;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 41 SALRSIPA 49
 Db 7 SALRSIPA 15

Db 11 SALRSIPA 19

RESULT 12
 US-08-379-613-5
 Sequence 5, Application US/08379613
 Patent No. 5736146
 GENERAL INFORMATION:
 APPLICANT: Cohen, Irun R.
 APPLICANT: Fridkin, Matityahu
 APPLICANT: Konen-Waisman, Stephanie
 TITLE OF INVENTION: Conjugates of Poorly Immunogenic
 TITLE OF INVENTION: Antigens and Synthetic Peptide Carriers and Vaccines
 TITLE OF INVENTION: Complicating Them.
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/379,613
 FILING DATE: 22-FEB-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Mirock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 7534-013-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..24
 OTHER INFORMATION: /label= Pep277S
 US-08-379-613-5

Query Match 33.3%; Score 40; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.037;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 41 SALRSIPA 49
 Db 6 SALRSIPA 14

RESULT 13
 US-08-324-297A-5
 Sequence 5, Application US/08324297A
 Patent No. 6174862
 GENERAL INFORMATION:
 APPLICANT: Brennenman, Douglas E.
 APPLICANT: Gozes, Ilana
 TITLE OF INVENTION: Neurotrophic Peptides of Activity
 TITLE OF INVENTION: Dependent Neurotrophic Factor
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Crew
 STREET: One Market Plaza, Stuart Street Tower

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,297A
FILING DATE: 17-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,973
FILING DATE: 22-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,087
FILING DATE: 22-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-178-1US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-324-297A-5
Query Match 30.0%; Score 36; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 42 ALLRSIPA 49
Db 1 ALLRSIPA 8
RESULT 14
US-08-324-297A-7
Sequence 7, Application US/08324297A
Patent No. 6174862
GENERAL INFORMATION:
APPLICANT: Breneman, Douglas E.
APPLICANT: Gozes, Illana
TITLE OF INVENTION: Neurotrophic Peptides of Activity
TITLE OF INVENTION: Dependent Neurotrophic Factor
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,297A
FILING DATE: 17-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,973
FILING DATE: 22-APR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,087
FILING DATE: 22-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-178-1US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-324-297A-7
Query Match 28.3%; Score 34; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 4.1e+05;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 41 SALLRSIPA 49
Db 1 TALLRSIPA 9
RESULT 15
US-09-248-796A-19008
Sequence 19008, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19008
LENGTH: 409
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-19008
Query Match 27.5%; Score 33; DB 4; Length 409;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 41 SALLRSIPA 49
Db 212 SALLRSIPA 220

Search completed: February 23, 2005, 19:36:08
Job time : 31.1695 secs

Result	No.	Score	Query #	Length	DB	ID	Description
1	40	33.3	9	9	US-09-267-511-1		Sequence 1, Appli
2	40	33.3	9	14	US-10-164-432-3		Sequence 3, Appli
3	40	33.3	9	15	US-10-296-849-9		Sequence 1, Appli
4	40	33.3	9	15	US-10-623-272-5		Sequence 5, Appli
5	40	33.3	9	15	US-10-623-272-6		Sequence 36, Appli
6	40	33.3	10	14	US-10-164-432-5		Sequence 3, Appli
7	40	33.3	10	15	US-10-296-849-19		Sequence 19, Appli
8	40	33.3	10	15	US-10-623-272-22		Sequence 22, Appli
9	40	33.3	11	15	US-10-296-849-18		Sequence 18, Appli
10	40	33.3	12	15	US-10-296-849-17		Sequence 17, Appli
11	40	33.3	13	15	US-10-296-849-16		Sequence 16, Appli
12	40	33.3	14	9	US-09-267-511-21		Sequence 21, Appli
13	40	33.3	14	14	US-10-164-432-6		Sequence 6, Appli

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Query Match Similarity      33.3%; Score 40; DB 9; Length 9;
Best Local Similarity      100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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QY 41 SALLRSIPA 49
Db 1 SALLRSIPA 9

RESULT 2

US-10-164-432-3
Sequence 3, Application US/10164432
Publication No. US20030166544A1
GENERAL INFORMATION:
APPLICANT: Alcon Inc.
APPLICANT: Clark, Abbot F.
APPLICANT: Debra, Shade L.
TITLE OF INVENTION: The Use of ADNF for the Treatment of Glaucomatous Optic Neuropath
FILE REFERENCE: 1975A US
CURRENT APPLICATION NUMBER: US/10/164,432
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: 09/921,029
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/230,964
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 9
TYPE: PRT
ORGANISM: homo sapiens
US-10-164-432-3

Query Match 33.3%; Score 40; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
Db 1 SALLRSIPA 9

RESULT 3

US-10-296-849-1
Sequence 1, Application US/10296849
Publication No. US20040048801A1
GENERAL INFORMATION:
APPLICANT: Spong, Catherine Y.
APPLICANT: Brennenman, Douglas
APPLICANT: Gozes, Ilana
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied and
APPLICANT: Industrial Development, Ltd.
TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
FILE REFERENCE: 15280W-004200US
CURRENT APPLICATION NUMBER: US/10/296,849
PRIOR FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/208,944
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: US 60/267,805
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: WO PCT/US01/17758
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Activity
OTHER INFORMATION: Dependent Neurotrophic Factor I (ADNF I) active
OTHER INFORMATION: core site, SAL or ADNF-9
US-10-296-849-1

Query Match 33.3%; Score 40; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
Db 1 SALLRSIPA 9

RESULT 4

US-10-623-272-5
Sequence 5, Application US/10623272
Publication No. US2004005313A1
GENERAL INFORMATION:
APPLICANT: Gozes, Ilana
APPLICANT: Brennenman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamoshtiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-291200US
CURRENT APPLICATION NUMBER: US/10/623,272
PRIOR FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF-9 active
OTHER INFORMATION: peptide antigen
US-10-623-272-5

Query Match 33.3%; Score 40; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
Db 1 SALLRSIPA 9

RESULT 5

US-10-623-272-36
Sequence 36, Application US/10623272
Publication No. US2004005313A1
GENERAL INFORMATION:
APPLICANT: Gozes, Ilana
APPLICANT: Brennenman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamoshtiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-291200US
CURRENT APPLICATION NUMBER: US/10/623,272
PRIOR FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF-9 active
OTHER INFORMATION: peptide adsorbed onto bovine serum albumin (BSA)
OTHER INFORMATION: as antigen
US-10-623-272-36

Query Match 33.3%; Score 40; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALURSIPIA 49
Db 1 SALURSIPIA 9

RESULT 6

US-10-164-432-5
Sequence 5, Application US/10164432
Publication No. US20030166544A1
GENERAL INFORMATION:
APPLICANT: Alcon Inc.
APPLICANT: Clark, Abbot F.
APPLICANT: Debra, Shade L.
TITLE OF INVENTION: The Use of ADNP for the Treatment of Glaucomatous Optic Neuropath
FILE REFERENCE: 1975A US
CURRENT APPLICATION NUMBER: US/10/164,432
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: 09/921,029
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 10
TYPE: PRT
ORGANISM: homo sapiens
US-10-164-432-5

Query Match 33.3%; Score 40; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALURSIPIA 49
Db 2 SALURSIPIA 10

RESULT 7

US-10-296-849-19
Sequence 19, Application US/10296849
Publication No. US20040048801A1
GENERAL INFORMATION:
APPLICANT: Spong, Catherine Y.
APPLICANT: Breneman, Douglas
APPLICANT: Gozes, Ilana
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied and
APPLICANT: Industrial Development, Ltd.
TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
FILE REFERENCE: 15280W-004200US
CURRENT APPLICATION NUMBER: US/10/296,849
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/208,944
PRIOR FILING DATE: 2000-05-31

PRIOR APPLICATION NUMBER: US 60/267,805
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: WO PCT/US01/17758
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF I
OTHER INFORMATION: polypeptide
US-10-296-849-19

Query Match 33.3%; Score 40; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALURSIPIA 49
Db 2 SALURSIPIA 10

RESULT 8

US-10-623-272-22
Sequence 22, Application US/10623272
Publication No. US20040053131A1
GENERAL INFORMATION:
APPLICANT: Gozes, Ilana
APPLICANT: Breneman, Douglas E.
APPLICANT: Baasman, Merav
APPLICANT: Zamostiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Actively Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-291200US
CURRENT APPLICATION NUMBER: US/10/623,272
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:peptide
OTHER INFORMATION: conjugated through the Cys residue to Sephadex for
OTHER INFORMATION: affinity chromatography
US-10-623-272-22

Query Match 33.3%; Score 40; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALURSIPIA 49
Db 2 SALURSIPIA 10

RESULT 9

US-10-296-849-18
Sequence 18, Application US/10296849
Publication No. US20040048801A1
GENERAL INFORMATION:
APPLICANT: Spong, Catherine Y.

APPLICANT: Brenneman, Douglas
APPLICANT: Gozes, Iilana
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied and
APPLICANT: Industrial Development, Ltd.
TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
FILE REFERENCE: 15280W-004200US
CURRENT APPLICATION NUMBER: US/10/296,849
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/208,944
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: US 60/267,805
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: WO PCT/US01/17758
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF I
US-10-296-849-18

Query Match 33.3%; Score 40; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 SALRSIPA 49
Db 3 SALRSIPA 11

RESULT 10
US-10-296-849-17
Sequence 17, Application US/10296849
Publication No. US20040048801A1
GENERAL INFORMATION:
APPLICANT: Brenneman, Douglas
APPLICANT: Gozes, Iilana
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied and
APPLICANT: Industrial Development, Ltd.
TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
FILE REFERENCE: 15280W-004200US
CURRENT APPLICATION NUMBER: US/10/296,849
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/208,944
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: US 60/267,805
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: WO PCT/US01/17758
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF I
US-10-296-849-17

Query Match 33.3%; Score 40; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.21;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 41 SALRSIPA 49
Db 4 SALRSIPA 12

RESULT 11
US-10-296-849-16
Sequence 16, Application US/10296849
Publication No. US20040048801A1
GENERAL INFORMATION:
APPLICANT: Spong, Catherine Y.
APPLICANT: Brenneman, Douglas
APPLICANT: Gozes, Iilana
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied and
APPLICANT: Industrial Development, Ltd.
TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
FILE REFERENCE: 15280W-004200US
CURRENT APPLICATION NUMBER: US/10/296,849
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/208,944
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: US 60/267,805
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: WO PCT/US01/17758
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF I
US-10-296-849-16

Query Match 33.3%; Score 40; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 SALRSIPA 49
Db 5 SALRSIPA 13

RESULT 12
US-09-267-511-21
Sequence 21, Application US/09267511
Patent No. US2002011301A1
GENERAL INFORMATION:
APPLICANT: Brenneman, Douglas E.
APPLICANT: Spong, Catherine Y.
APPLICANT: Gozes, Iilana
APPLICANT: Basaan, Merav
APPLICANT: Zamoshtano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied Research
APPLICANT: and Industrial Development, Ltd.
TITLE OF INVENTION: Prevention of Petal Alcohol Syndrome and Neuronal Cell
TITLE OF INVENTION: Death with ADNF Polypeptides
FILE REFERENCE: 015280-377000US
CURRENT APPLICATION NUMBER: US/09/267,511
CURRENT FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21

LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF I
US-09-267-511-21

Query Match 33.3%; Score 40; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
Db 6 SALLRSIPA 14

RESULT 13
US-10-164-432-6
Sequence 6, Application US/10164432
Publication No. US20030166544A1
GENERAL INFORMATION:
APPLICANT: Alcon Inc.
APPLICANT: Clark, Abbot F.
APPLICANT: Debra, Shade L.
TITLE OF INVENTION: The Use of ADNF for the Treatment of Glaucomatous Optic Neuropath
FILE REFERENCE: 1975A US
CURRENT APPLICATION NUMBER: US/10/164,432
CURRENT FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: 09/921,029
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/230,964
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 14
TYPE: PRT
ORGANISM: homo sapiens
US-10-164-432-6

Query Match 33.3%; Score 40; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
Db 6 SALLRSIPA 14

RESULT 14
US-10-296-849-14
Sequence 14, Application US/10296849
Publication No. US20040048801A1
GENERAL INFORMATION:
APPLICANT: Spong, Catherine Y.
APPLICANT: Breneman, Douglas
APPLICANT: Gozes, Iliana
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied and
APPLICANT: Industrial Development, Ltd.
TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
FILE REFERENCE: 15280W-004200US
CURRENT APPLICATION NUMBER: US/10/296,849
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/208,944
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: US 60/267,805
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: WO PCT/US01/17758
PRIOR FILING DATE: 2001-05-31

NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF I
US-10-296-849-14

Query Match 33.3%; Score 40; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
Db 6 SALLRSIPA 14

RESULT 15
US-10-623-272-23
Sequence 23, Application US/10623272
Publication No. US2004005313A1
GENERAL INFORMATION:
APPLICANT: Gozes, Iliana
APPLICANT: Breneman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamoshtiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-291200US
CURRENT APPLICATION NUMBER: US/10/623,272
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:active peptide
US-10-623-272-23

Query Match 33.3%; Score 40; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
Db 6 SALLRSIPA 14

Search completed: February 23, 2005, 19:51:27
Job time : 90 secs

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QY 42 ALRSLIPA 49
DB 519 AMRSLIPA 526

RESULT 3

C86825
uracil permease [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C/Accession: C86825
R/Bolotin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s8
A/Reference number: A86623; MUID:21235186; PMID:11337471
A/Accession: C86825
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-430 <STO>
A/Cross-references: UNIPROT:Q9CF78; GB:AE005176; PID:912724609; PIDN:AAK05701.1; GSPDB:C
A/Experimental source: strain IL1403
C/Genetics:
A/Gene: pyrP
C/Superfamily: uracil transport protein ura

Query Match 27.5%; Score 33; DB 2; Length 430;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALRSLIPA 49
DB 339 TALRSLIPA 347

RESULT 4

A59266
unconventional myosin-15 - human
C/Species: Homo sapiens (hmn)
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C/Accession: A59266
R/Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; M
an, T.B.; Friedell, R.A.
Genomics 61, 243-258, 1999
A/Title: Characterization of the human and mouse unconventional myosin XV genes responsi
A/Reference number: A59266; MUID:20021762; PMID:10552926
A/Accession: A59266
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-3530 <LTA>
A/Cross-references: UNIPROT:Q9UKN7; GB:AF144094; NID:G6224682; PIDN:AAF05903.1; PID:G622
F,1225-1887/Domain: myosin motor domain homology <MMO>

Query Match 27.5%; Score 33; DB 2; Length 3530;
Best Local Similarity 77.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 SALRSLIPA 49
DB 2482 SALRSLIPA 2490

RESULT 5

D86518
hypothetical protein CPJ0220 [imported] - Chlamydomonada pneumoniae (strain J138)
C/Species: Chlamydomonada pneumoniae, Chlamydia pneumoniae
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: D86518
R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
A/Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A/Reference number: A86491; MUID:20330349; PMID:10871362
A/Accession: D86518

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-181 <STO>
A/Cross-references: UNIPROT:Q9Z8M4; GB:BA000008; NID:G8978593; PIDN:BA098430.1; GSPDB:G
A/Experimental source: strain J138
C/Genetics:
A/Gene: CPJ0220

Query Match 26.7%; Score 32; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 ALRSLIP 48
DB 52 ALRSLIP 58

RESULT 6

C72104
hypothetical protein CP0545 [imported] - Chlamydomonada pneumoniae (strain CWL029 and A
C/Species: Chlamydomonada pneumoniae, Chlamydia pneumoniae
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: C72104; B81567
R/Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21, 385-389, 1999
A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A/Reference number: A72000; MUID:99206606; PMID:10192388
A/Accession: C72104
A/Molecule type: DNA
A/Residues: 1-181 <ARN>
A/Cross-references: UNIPROT:Q9Z8M4; GB:AE001608; GB:AE001363; NID:94376487; PIDN:AD183
A/Experimental source: strain CWL029
C/Genetics:
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gilm, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of Chlamydia trachomatis MOPn and Chlamydia pneumoniae AR39.
A/Reference number: A81500; MUID:20150255; PMID:10684935
A/Accession: B81567
A/Molecule type: DNA
A/Residues: 1-181 <REA>
A/Cross-references: GB:AE002213; GB:AE002161; NID:G7189446; PIDN:AAF38367.1; PID:G71894
A/Experimental source: strain AR39, HL cells
C/Genetics:
A/Gene: CP0220; CP0545

Query Match 26.7%; Score 32; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 ALRSLIP 48
DB 52 ALRSLIP 58

RESULT 7

H82148
amino acid ABC transporter, permease protein VC1861 [imported] - Vibrio cholerae (strain
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: H82148
R/Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gilm, M.L.; Dodson, R.J.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bess, S.; Qin, H.; Dragol, I.; Sellers,
I.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: H82148
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-225 <HET>
A/Cross-references: UNIPROT:Q9KQY6; GB:AE004261; GB:AE003852; NID:99656382; PIDN:AAF950
A/Experimental source: serogroup O1, strain N16961; biotype El Tor
C/Genetics:

A;Gene: VC1861
A;Map position: 1
C;Superfamily: histidine permease protein M

Query Match 26.7%; Score 32; DB 2; Length 225;
Best Local Similarity 77.8%; Pred. No. 24;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 SALRSIPA 49
DB 143 SALRSIPA 151

RESULT 8

S61660

probable membrane protein YOR100C - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: hypothetical protein OJ193; hypothetical protein YOK3193C

C;Species: *Saccharomyces cerevisiae*

C;Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 19-Apr-2002

C;Accession: S61660; S66985

R;Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banrevel, A.; Sander, C.; Valencia

submitted to the EMBL Data Library, December 1995

A;Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome

A;Reference number: S61643

A;Accession: S61660

A;Molecule type: DNA

A;Residues: 1-327 <BEN>

A;Cross-references: EMBL:X94335; NID:G1262139; PID:G1164947

R;Voss, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansoorge, W.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S66985

A;Accession: S66985

A;Molecule type: DNA

A;Residues: 1-327 <VOS>

A;Cross-references: EMBL:Z75008; NID:G1420278; PID:G1420279; MIPS:YOR100C

C;Experimental source: strain S288C

C;Genetics:

A;Gene: SGD:CRCL

A;Cross-references: SGD:S0005626

A;Map position: 15R

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C;Keywords: transmembrane protein

F;3-137/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;101-117/Domain: transmembrane #status predicted <TM1>

F;138-222/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F;236-322/Domain: ADP,ATP carrier protein repeat homology <ACP3>

F;242-258/Domain: transmembrane #status predicted <TM2>

Query Match 26.7%; Score 32; DB 2; Length 327;
Best Local Similarity 87.5%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 42 ALLRSIPA 49
DB 300 ALLRSIPA 307

RESULT 9

F72331

conserved hypothetical protein - *Thermotoga maritima* (strain MSB8)

C;Species: *Thermotoga maritima*

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: F72331

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Accession: F72331

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-330 <ARN>

A;Cross-references: UNIPROT:Q9WZS0; GB:AE001748; GB:AE000512; NID:G4981332; PID:AA0358
A;Experimental source: strain MSB8
C;Genetics:

A;Gene: TM0813

Query Match 26.7%; Score 32; DB 2; Length 330;
Best Local Similarity 66.7%; Pred. No. 35;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 41 SALRSIPA 49
DB 295 SALRSIPA 303

RESULT 10

C72424

oligopeptide ABC transporter, ATP-binding protein - *Thermotoga maritima* (strain MSB8)

C;Species: *Thermotoga maritima*

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: C72424

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: C72424

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-331 <ARN>

A;Cross-references: UNIPROT:Q9WXR4; GB:AE001692; GB:AE000512; NID:G4980535; PID:AA0351

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM0058

C;Superfamily: inner membrane protein malK; ATP-binding cassette homology

F;24-237/Domain: ATP-binding cassette homology <ABC>

Query Match 26.7%; Score 32; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 ALLRSIP 48
DB 259 ALLRSIP 265

RESULT 11

A84387

oligopeptide ABC transporter ATP-binding [imported] - *Halobacterium* sp. NRC-1

C;Species: *Halobacterium* sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: A84387

R;Ng, W.V.; Kennedy, S.P.; Mahairs, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,

Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl

Jung, K.H.; Alam, M.; Freilias, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; L

A;Title: Genome sequence of *Halobacterium* species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: A84387

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-440 <SNO>

A;Cross-references: UNIPROT:Q9HMMO; GB:AE004437; NID:G10581771; PID:AMG20461.1; GSPDB:

C;Genetics:

A;Gene: appf

Query Match 26.7%; Score 32; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 ALLRSIP 48

Db 265 ALRSIP 271

RESULT 12

E64120
exodeoxyribonuclease I (EC 3.1.11.1) - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C/Accession: E64120
R/Reichmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A./Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:95350630; PMID:7542800
A/Accession: E64120
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-473 <TIGR>
A/Cross-references: UNIPROT:P45188; GB:U32818; GB:L42023; NID:91574209; PIDN:AAC23023.1;
C/Superfamily: exodeoxyribonuclease I
C/Keywords: DNA repair; hydrolase

Query Match 26.7%; Score 32; DB 2; Length 473;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 42 ALRSIP 49
Db 379 ALRSIP 386

RESULT 13

S11035
chaperonin hsp60, testis - tobacco budworm
C/Species: Heliothis virescens (tobacco budworm)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S11035
R/Miller, S.G.; Leclerc, R.F.; Erdos, G.W.
J. Mol. Biol. 214, 407-422, 1990
A/Title: Identification and characterization of a testis-specific isoform of a chaperonin
A/Reference number: S11035; MUID:90339485; PMID:1974308
A/Accession: S11035
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-569 <JMC>
A/Cross-references: UNIPROT:P25420; GB:X56034; NID:9296831; PIDN:CAA39509.1; PID:9296832
A/Note: the sequence from Fig. 8 is inconsistent with that from Fig. 6 in having 45-Glu
C/Superfamily: chaperonin groEL

Query Match 26.7%; Score 32; DB 2; Length 569;
Best Local Similarity 77.8%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 SALRSIP 49
Db 444 ALRSIP 452

RESULT 14

E70037
serine O-acetyltransferase homolog yvfd - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: E70037
R/Kunet, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte, C.; Bron, S.; Brouillet, S.; Bruchet, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Erttington, J.; Fabret, C.; Ferrati, E.
Nature 390, 249-256, 1997
A/Authors: Foulgier, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallet, I.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecell, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanton, A/Authors: Schleich, S.; Schroeder, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Sero, Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetre, P.; Tognoni, A.; Tosa, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: E70037
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-216 <KDN>
A/Cross-references: UNIPROT:P71063; GB:Z99121; GB:AL009126; NID:92635827; PIDN:CB15429
A/Experimental source: strain 168
C/Genetics:
A/Gene: yvfd

Query Match 25.8%; Score 31; DB 2; Length 216;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALRSIP 48
Db 187 SALRSIP 194

RESULT 15

C84798
hypothetical protein At2g37880 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: C84798
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Ko, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Umayam, L.; Tallon, L. euse, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, A.
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: C84798
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-247 <STO>
A/Cross-references: UNIPROT:Q7XJQ1; GB:AE002093; NID:94895196; PIDN:AAD32783.1; GSPDB:G
A/Genetics:
A/Gene: At2g37880
A/Map position: 2

Query Match 25.8%; Score 31; DB 2; Length 247;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 SALRSIP 48
Db 142 SALRSIP 149

Search completed: February 23, 2005, 19:35:03
Job time : 27.6384 secs


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RP SEQUENCE FROM N.A.
RA Vadelette F., Male R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.
DR EMBL; AY049960; AAL2931.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:00051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR Pfam; PF00118; Cpn60_TGPI.1.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
DR ATP-binding; Chaperone; Heat shock.
FT NON_TER 1
FT NON_TER 167
SQ SEQUENCE 167 AA; 17350 MW; 2D6DA1D962C7634 CRC64;

Query Match
Best Local Similarity 30.0%; Score 36; DB 2; Length 167;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 ALTRSLPA 49
DB 53 ALTRSLPA 60

RESULT 3
Q8RXW5 PRELIMINARY; PRT; 223 AA.
AC Q8RXW5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein At4g26430 (fragment).
GN Name:At4g26430;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY080638; AAL85984.1; -.
DR InterPro; IPR000555; Mov34_MFN_PAD1.
DR Pfam; PF01398; Mov34; 1.
DR Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 223 AA; 25181 MW; 64892BB860166D7B CRC64;

Query Match
Best Local Similarity 29.2%; Score 35; DB 2; Length 223;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALRSLPA 49
DB 158 SALRSLPA 166

RESULT 4
O65591 PRELIMINARY; PRT; 286 AA.
ID O65591;
AC O65591;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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DE Hypothetical protein M3B9.140 (Hypothetical protein At4g26430).
GN Name:M3B9.140; Synonym=At4g26430;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Vandenberg M., Jallet C., Portetelle D., Hohnsels J.,
RA Mewes H.W., Mayer K.F.X., Lemcke K., Scheller C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Vandenberg M., Jallet C., Portetelle D., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022223; CA18227.1; -.
DR EMBL; AL161565; CAB79498.1; -.
DR PIR; T05061; T05061.
DR InterPro; IPR003639; Mov34-1.
DR InterPro; IPR000555; Mov34_MFN_PAD1.
DR Pfam; PF01398; Mov34; 1.
DR ProDom; PD363422; Mov34-1; 1.
DR SMART; SM00232; JAB_MFN; 1.
KW Hypothetical protein.
SQ SEQUENCE 286 AA; 31954 MW; 51008C281F029684 CRC64;

Query Match
Best Local Similarity 29.2%; Score 35; DB 2; Length 286;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALRSLPA 49
DB 221 SALRSLPA 229

RESULT 5
O8W205 PRELIMINARY; PRT; 317 AA.
ID O8W205;
AC O8W205;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CSN complex subunit 6B (Transcription factor-like) (Hypothetical
DE protein At4g26430).
GN Name:CSN6B; Synonym=At4g26430;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21607801; PubMed=11742986; DOI=10.1093/emboj/20.24.7096;
RA Fu H., Reis N., Lee Y., Glickman M.H., Vierstra R.;
RT "Subunit interaction maps for the regulatory particle of the 26S
RT proteasome and the COP9 signalosome."
RL EMBO J. 20;7096-7107(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome

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RT annotation." ;
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).
 [3]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.,
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA Omidera C.S., Quach H.L., Tang C.C., Toriumi M., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
 RA Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
 RA Becker J.R., Theologis A.,
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF395064; AAL58107.1; -
 DR EMBL: AF087556; AAL65098.1; -
 DR EMBL: BT002345; AAN86178.1; -
 DR Pfam: PF01396; Mov34; 1.
 DR ProDom: PD363422; Mov34-1; 1.
 DR SMART: SM00232; JAB_MPV; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 317 AA; 35404 MW; 9629A50F9EDA2C0B CRC64;

Query Match 29.2%; Score 35; DB 2; Length 317;
 Best Local Similarity 77.8%; Pred. No. 52;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 41 SALRSIPA 49
 Db 252 SSLRLSLPA 260

RESULT 6
 O8MW1P0 PRELIMINARY; PRT; 318 AA.
 AC O8MW1P0;
 DT 01-MAR-2002 (TRENBLREL. 20, Created)
 DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
 DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
 GN COP9 signalosome subunit 6.
 DN Name=C9NB;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2158789; PubMed=11701877;
 RA Peng Z., Serino G., Deng X.W.;
 RT "Molecular characterization of subunit 6 of the COP9 signalosome and
 its role in multifaceted developmental processes in Arabidopsis.";
 RL Plant Cell 13:2393-2407 (2001).
 DR EMBL: AF34762; AAL49561.1; -
 DR Pfam: PF01398; Mov34; 1.
 DR ProDom: PD363422; Mov34-1; 1.
 DR SMART: SM00232; JAB_MPV; 1.
 SQ SEQUENCE 318 AA; 35493 MW; 6AA06F21C8AEFA29 CRC64;

Query Match 29.2%; Score 35; DB 2; Length 318;
 Best Local Similarity 77.8%; Pred. No. 52;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 41 SALRSIPA 49
 Db 253 SSLRLSLPA 261

RESULT 7
 O8SFX2 PRELIMINARY; PRT; 157 AA.
 ID O8SFX2
 AC O8SFX2;

DT 01-JUN-2002 (TRENBLREL. 21, Created)
 DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE Cytochrome b (Fragment).
 GN Name=Cytb;
 OS Cherax tenuimanus (Australian crayfish).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Parastacidae; Parastacidae; Cherax.
 OX NCBI_TaxID=99755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Munsinghe D.H.N., Murphy N.P., Austin C.M.;
 RT "Utility of mitochondrial DNA sequences from four gene regions for
 systematic studies of Australian freshwater crayfish of the genus
 Cherax (Decapoda: Parastacidae)." ;
 RL J. Crust. Biol. 23:402-417 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Munsinghe H.N., Murphy N.P., Austin C.M.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Munsinghe H.N., Austin C.M., Whisson G.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Component of the ubiquinol-cytochrome c reductase
 complex (complex III or cytochrome b-c1 complex), which is a
 respiratory chain that generates an electrochemical potential
 coupled to ATP synthesis (By similarity).
 CC -1- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
 b562) is low-potential and absorbs at about 562 nm, and heme 2 (or
 BH or b566) is high-potential and absorbs at about 566 nm (By
 similarity).
 CC -1- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
 cytochrome c1 and the Rieske protein (By similarity).
 CC -1- SIMILARITY: Belongs to the cytochrome b family.
 DR EMBL: AF492797; AAM43682.1; -
 DR EMBL: AF510177; AAM44277.1; -
 DR EMBL: AF510179; AAM44279.1; -
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0005746; C: mitochondrial electron transport chain; IEA.
 DR GO: GO:0005739; C: mitochondrion; IEA.
 DR GO: GO:0016491; F: oxidoreductase activity; IEA.
 DR GO: GO:0006418; P: electron transport; IEA.
 DR GO: GO:0006410; P: transport; IEA.
 DR InterPro: IPR005798; Cytb_b6_C.
 DR InterPro: IPR005797; Cytb_b6_N.
 DR Pfam: PF00032; Cytochrom_B_C; 1.
 DR Pfam: PF00033; Cytochrom_B_N; 1.
 DR PROSITE: PS00193; CYTOCHROME_B_OO; UNKNOWN 1.
 KW Electron transport; Heme; Mitochondrion; Respiratory chain;
 KW Transmembrane; Transport.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 157 AA; 17653 MW; 8E7A8ABDB70FE70 CRC64;

Query Match 28.3%; Score 34; DB 2; Length 157;
 Best Local Similarity 87.5%; Pred. No. 40;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 41 SALRSIPA 48
 Db 145 SALRSIPA 152

RESULT 8
 O9GBG9 PRELIMINARY; PRT; 379 AA.
 ID O9GBG9
 AC O9GBG9;
 DT 01-MAR-2001 (TRENBLREL. 16, Created)
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)

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DE Cytochrome b.
GN Name=cytb;
OS Mustela altaica (mountain weasel).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Euteleia; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=92062;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21138802; Pubmed=11245219;
RA Hosoda T., Suzuki H., Harada M., Tsuchiya K., Han S.H., Zhang Y.,
RA Kryukov A.P., Lin L.K.;
RT "Evolutionary trends of the mitochondrial lineage differentiation in
RT species of genera Martes and Mustela."
RL Genet. Syst. 75:259-267(2000).
CC -1- FUNCTION. Component of the ubiquinol-cytochrome c reductase
CC complex (complex III or cytochrome b-c1 complex), which is a
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -1- COFACTOR. Binds two heme groups non-covalently. Heme 1 (or BL or
CC b562) is low-potential and absorbs at about 562 nm, and heme 2 (or
CC BH or b566) is high-potential and absorbs at about 566 nm (By
CC similarity).
CC -1- SUBUNIT. The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC -1- SIMILARITY. Belongs to the cytochrome b family.
DR EMBL; AB051239; BAB18191.1; -.
DR HSSP; P00157; 1B3.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR005798; Cytb_b6_N.
DR InterPro; IPR005797; Cytb_b6_C.
DR Pfam; PF00032; Cytochrom_B_C_1.
DR Pfam; PF00033; Cytochrom_B_N_1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME, 1.
DR PROSITE; PS00193; CYTOCHROME_B_QQ; UNKNOWN_1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane; Transport.
SQ SEQUENCE 379 AA; 42590 MW; 435AF969C998960B CRC64;

Query Match 28.3%; Score 34; DB 2; Length 379;
Best Local Similarity 87.5%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 42 ALRSIPA 49
DB 279 ALRSIPA 286

RESULT 9
OBA9X9 PRELIMINARY; PRT; 394 AA.
ID OBA9X9;
AC OBA9X9;
DT 01-JUN-2003 (TRENBLREL. 24, Created)
DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Putative uracil permease (Uracil transporter).
GN OrderedLocustNames=BR0686;
OS Bacteroides thetaiotaomicron.
OC Bacteriia; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteriodes.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550898; Pubmed=12663928; DOI=10.1126/science.1080029;
RX Xu J., Bjursell M.K., Himrod U., Deng S., Carmichael L.K.,
RX Chiang H.C., Hooper L.V., Gordon J.I.;

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RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
RL EMBL; AE016928; AA075793.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006043; Xant/urac/vitC.
DR InterPro; IPR006042; Xan ur permease.
DR Pfam; PRO0860; Xan ur permease; 1.
DR TIGRfam; TIGR00801; nce2; 1.
DR PROSITE; PS01116; XANTH_URACIL_PERMASE; 1.
KW Complete proteome.
SQ SEQUENCE 394 AA; 41238 MW; AF6D88BF79D84FC9 CRC64;

Query Match 28.3%; Score 34; DB 2; Length 394;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALKSIPA 49
DB 307 SALKSIPS 315

RESULT 10
O64UD6 PRELIMINARY; PRT; 395 AA.
ID O64UD6;
AC O64UD6;
DT 25-OCT-2004 (TRENBLREL. 28, Created)
DT 25-OCT-2004 (TRENBLREL. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLREL. 28, Last annotation update)
DE Putative uracil permease.
GN ORFNames=BF2146;
OS Bacteroides fragilis.
OC Bacteriia; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteriodes.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kohara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation."
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
DR EMBL; AP006841; BAD48893.1; -.
SQ SEQUENCE 395 AA; 41513 MW; 72C693370D25865D CRC64;

Query Match 28.3%; Score 34; DB 2; Length 395;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALKSIPA 49
DB 307 SALKSIPS 315

RESULT 11
O73MJ6 PRELIMINARY; PRT; 422 AA.
ID O73MJ6;
AC O73MJ6;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Membrane protein, putative.
GN OrderedLocustNames=RD81512;
OS Treponema denticola.
OC Bacteriia; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 35405 / DSM 14222;
RX Pubmed=1564399; DOI=10.1073/pnas.0307639101;
RX Sehnadi R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.;

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RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
 RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
 RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
 RA Gargaregis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
 RA Shatman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
 RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
 RA Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.,
 RT "Comparison of the genome of the oral pathogen *Treponema denticola*
 RT with other spirochete genomes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
 DR EMBL: AE017251; AAS12029.1; -.
 DR TIGR: TDB1512; -.
 KW Complete proteome.
 SQ SEQUENCE 422 AA; 48017 MW; 525219A73FD8588E CRC64;
 Query Match 28.3%; Score 34; DB 2; Length 422;
 Best Local Similarity 87.5%; Pred. No. 1.2e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALRSIP 48
 |||
 Db 58 SALRSIP 65

RESULT 12
 Q8XK98 PRELIMINARY; PRT; 432 AA.
 AC Q8XK98;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Probable uracil permease.
 GN Name:uraA; OrderedLocustNames=CPE1505;
 OS *Clostridium perfringens*.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13;
 RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
 RT "Complete genome sequence of *Clostridium perfringens*, an anaerobic
 RT flesh-eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).
 DR EMBL: AP003190; BAB81211.1; -.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005215; F:transporter activity; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR Pfam: PF00860; Xan ur permease; 1.
 DR TIGRFAMs: TIGR00801; ncs2; 1.
 DR PROSITE: PS0116; XANTH_UAPCIT_PERMASE; 1.
 KW Complete proteome.
 SQ SEQUENCE 432 AA; 45695 MW; 2E732D28AAE155A2 CRC64;
 Query Match 28.3%; Score 34; DB 2; Length 432;
 Best Local Similarity 87.5%; Pred. No. 1.2e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALRSIP 48
 |||
 Db 337 SALRSIP 344

RESULT 13
 Q7S970 PRELIMINARY; PRT; 444 AA.
 AC Q7S970;
 DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical protein.

GN Name=NCU07298.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selltremlkoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Koche G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
 RA Kamal M., Kamysellis M., Mauceli E., Bielke C., Rudd S., Frisman D.,
 RA Kyrstofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
 RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
 RA Yarden O., Plamann M., Selter S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Manhaupt G., Ebbole D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nisbaum C., Birren B.,
 RT "The Genome Sequence of the Filamentous Fungus *Neurospora crassa*.";
 RL Nature 0:0-0 (2003).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AABX01000217; EAA32916.1; -.
 DR HSPSP; P77407; IPOY.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR003673; CAIB_BAIF.
 DR Pfam: PF02515; COA_transf_3; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 444 AA; 46688 MW; 07C93D806E3106FD CRC64;
 Query Match 28.3%; Score 34; DB 2; Length 444;
 Best Local Similarity 88.9%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 SALRSIPA 49
 |||
 Db 13 SALRSIPA 21

RESULT 14
 Q9L423 PRELIMINARY; PRT; 642 AA.
 AC Q9L423;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Serine/threonine kinase.
 GN Name=PKNC;
 OS *Anabaena* sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC 7120;
 RA Gonzalez L., Phalip V., Zhang C.C.,
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ251821; CAB75357.1; -.
 DR PhosSite: Q9L423; -.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004672; F:protein kinase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011009; Kinase_1like.
 DR InterPro: IPR000719; Prot kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot kinase; 1.
 DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
 KW Kinase.
 SQ SEQUENCE 642 AA; 70785 MW; 81B36952C869EB67 CRC64;

Query Match 28.3%; Score 34; DB 2; Length 642;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 42 ALRSIPA 49
 |:|||||
 DB 519 AMRSIPA 526

RESULT 15

Q8YMW1 PRELIMINARY; PRT; 642 AA.
 ID O8YMW1
 AC O8YMW1
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Serine/threonine kinase.
 GN Name=pkc; OrderedLocNames=all14813;
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 CX NCBI_TaxID=103690;
 RX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriyuchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.,
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120."
 RL DNA Res. 8:205-213(2001).
 DR EMBL; AP003597; BAB76512.1; -.
 DR PIR; AE2407.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004672; F:protein kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR Pfam; PF00069; Pkinase; 1.
 DR Prodom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Complete proteome; Kinase.
 SQ SEQUENCE 642 AA; 70834 MW; DBA9C8F3D27847AA CRC64;

Query Match 28.3%; Score 34; DB 2; Length 642;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 42 ALRSIPA 49
 |:|||||
 DB 519 AMRSIPA 526

Search completed: February 23, 2005, 19:34:16
 Job time : 125.65 secs

CC polynucleotide in biological samples, while the antibodies are useful
 CC therapeutically and to isolate ADNF III polypeptides
 XX
 SQ Sequence 8 AA;

Query Match 33.9%; Score 41; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 41 NAPVSIPQ 48
 |||||
 1 NAPVSIPQ 8

RESULT 2
 ID AAW64678 standard; protein; 8 AA.
 XX
 AC AAW64678;
 XX
 DT 04-NOV-1998 (first entry)
 XX
 DE Human ADNF-III derived active peptide #2.

XX Activity dependent neurotrophic factor III: ADNF-III; ADNF; cell death;
 KW activity dependent neuroprotective protein; neurone; excitotoxicity;
 KW spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;
 KW N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
 XX HIV infection.
 OS Synthetic.

XX Key
 FT Modified-site
 FT 1 Location/Qualifiers
 FT /note= "N-terminal Asn is modified by the presence of an
 FT (R1)x group where R1 is an amino acid sequence of 1 to 40
 FT amino acids wherein each amino acid is independently
 FT selected from a group consisting of naturally occurring
 FT amino acids and amino acid mimetics"
 FT 8
 FT Modified-site
 FT /note= "C-terminal Gln is modified by the presence of an
 FT (R2)y group where R2 is an amino acid sequence of 1 to 40
 FT amino acids wherein each amino acid is independently
 FT selected from a group consisting of naturally occurring
 FT amino acids and amino acid mimetics"

XX MO9835042-A2.
 XX 13-AUG-1998.
 XX
 XX 06-FEB-1998; 98MO-US002485.
 XX
 XX 07-FEB-1997; 97US-0037404P.
 XX
 XX (USSH) US SEC HEALTH & HUMAN SERVICES.
 XX
 XX Gozes I, Brenneman DE, Bassan M;
 XX WPI, 1998-447239/38.
 XX

PT Activity dependent neurotrophic factor III polypeptide - useful
 PT therapeutically to prevent neuronal cell death associated with e.g. HIV
 PT infection, excitotoxicity or Alzheimer's disease.
 XX

PS Claim 24; Page 6; 121pp; English.

XX This sequence represents a peptide used in a method which isolates a
 CC novel activity dependent neurotrophic factor III. ADNF-III (also known as
 CC activity dependent neuroprotective protein, ADNP). ADNF III polypeptides
 CC can be used to prevent neuronal cell death, of e.g. the spinal cord,
 CC hippocampal, cerebral cortical or cholinergic neurones associated with
 CC e.g. HIV infection, excitotoxicity induced by N-methyl-D-aspartate
 CC stimulation or beta-amyloid peptide in Alzheimer's disease. The

CC polypeptides can also be combined with a carrier to alleviate learning
 CC impairment produced by cholinergic blockade in Alzheimer's patients. The
 CC nucleic acids are useful in polypeptide production and to detect ADNF III
 CC polynucleotide in biological samples, while the antibodies are useful
 CC therapeutically and to isolate ADNF III polypeptides
 XX
 SQ Sequence 8 AA;

Query Match 33.9%; Score 41; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 41 NAPVSIPQ 48
 |||||
 1 NAPVSIPQ 8

RESULT 3
 ID AAY71143 standard; peptide; 8 AA.
 XX
 AC AAY71143;
 XX
 DT 08-SEP-2000 (first entry)
 XX
 DE Human ADNF III-8 or NAP peptide sequence, NAPVSIPQ.

XX Activity Dependent Neurotrophic Factor III; ADNF; human; ADNP; NAP;
 KW Activity Dependent Neuroprotective Protein; chromosome 20q13.2; ADNPLE;
 KW autosomal dominant nocturnal frontal-lobe epilepsy; neuronal cell death;
 KW neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;
 KW Alzheimer's disease; beta-amyloid peptide; Huntington's disease;
 KW epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;
 KW amyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;
 KW mitochondrial abnormality; Wernicke's encephalopathy; homocystinuria;
 KW hyperproliferia; sulphite oxide disease; Tourette's syndrome; noctropic;
 KW Down's syndrome; drug addiction; developmental retardation; antileptic;
 KW learning impairment; anticonvulsant; neuroprotective; anti-HIV.

XX Homo sapiens.
 OS
 XX MO200027875-A2.
 XX
 XX 18-MAY-2000.
 XX
 XX 04-NOV-1999; 99MO-US026213.
 XX
 XX 06-NOV-1998; 98US-00187330.
 XX
 XX (USAS) GOVERNMENT US REPRESENT AS.
 XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 XX
 XX Gozes I, Brenneman DE, Bassan M, Zamostiano R;
 XX WPI, 2000-376491/32.
 XX

PT New nucleic acid encoding an activity dependent neurotrophic factor III
 PT (ADNF III) useful in the treatment of neurological deficiencies and for
 PT preventing neuronal cell death.
 XX

PS Example; Page 5; 136pp; English.

XX The present sequence is the human Activity Dependent Neurotrophic Factor
 CC (ADNF) III-8 or NAP peptide sequence. This peptide was synthesised based
 CC on the structural homology to ADNF-9 active peptide and hsp60. It is also
 CC used as an antigen for immunological detection of cloned ADNF III. ADNF
 CC III is also called an Activity Dependent Neuroprotective Protein (ADNP).
 CC The human gene was mapped to chromosome 20q13.2 and is linked to
 CC autosomal dominant nocturnal frontal-lobe epilepsy (ADNPLE) gene. It is
 CC expressed in the astrocytes, brain and also in foetal lung and endocrine
 CC tissues. This sequence has homology to ADNF I and hsp60, heat shock
 CC protein and PIFI, a DNA repair protein. The ADNF III polypeptides are
 CC useful for the treatment of neurological deficiencies and for prevention

CC of neuronal cell death associated with gp120, the envelope protein from
 CC HIV; N-methyl-D-Aspartic acid (excito-toxicity); tetrodotoxin (blockage
 CC of electrical activity); and beta-amyloid peptide, a substance related to
 CC neuronal degeneration in Alzheimer's disease. It is useful for the
 CC treatment of Huntington's disease, AIDS dementia complex, epilepsy,
 CC neuropathic pain syndromes, Parkinson's disease, amyotrophic lateral
 CC sclerosis (ALS), mitochondrial abnormalities, Leber's disease, Werhlicke's
 CC encephalopathy, Alzheimer's disease, homocysteinuria, hyperproliferia,
 CC sulphite oxide disease, Tourette's syndrome, oxidative stress induced
 CC neuronal death, Down's syndrome, developmental retardation and learning
 CC impairments, drug addiction, tolerance and dependency

CC Sequence 8 AA:

Query Match 33.9%; Score 41; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NBPVSIPQ 48
 |||||
 DB 1 NBPVSIPQ 8

RESULT 4
 AAB23470
 ID AAB23470 standard; peptide; 8 AA.

XX AAB23470;

DT 22-JAN-2001 (first entry)

XX Activity dependent neurotrophic factor I peptide #2.

XX Activity dependent neurotrophic factor; ADNF; FAS;

KM foetal alcohol syndrome; gene therapy; neurological deficiency;

XX neuronal cell death.

XX Unidentified.

XX WO200053217-A2.

XX 14-SEP-2000.

XX 10-MAR-2000; 2000WO-US006364.

XX 12-MAR-1999; 99US-00267511.

XX (UTRA-) UNIV RAMOT.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Breneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;

XX WPI; 2000-601940/57.

XX Treating condition associated with fetal alcohol syndrome in a subject

XX exposed to alcohol in utero or reducing neuronal death, involves

XX administering activity dependent neurotrophic factors I and/or III.

XX Claim 9; Page 51; 65pp; English.

XX The present invention relates to the treatment of a condition associated

XX with foetal alcohol syndrome (FAS), involving administering an activity

XX dependent neurotrophic factor (ADNF). ADNFs of the present invention may

XX also be used to treat neurological deficiencies and prevent neuronal cell

XX death. The present sequence is an ADNF peptide

XX Sequence 8 AA:

QY

DB |||||
 1 NBPVSIPQ 8

RESULT 5
 AAB23472
 ID AAB23472 standard; peptide; 8 AA.

XX AAB23472;

DT 22-JAN-2001 (first entry)

XX Activity dependent neurotrophic factor I peptide #4.

XX Activity dependent neurotrophic factor; ADNF; FAS;

KM foetal alcohol syndrome; gene therapy; neurological deficiency;

XX neuronal cell death.

XX Unidentified.

XX WO200053217-A2.

XX 14-SEP-2000.

XX 10-MAR-2000; 2000WO-US006364.

XX 12-MAR-1999; 99US-00267511.

XX (UTRA-) UNIV RAMOT.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Breneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;

XX WPI; 2000-601940/57.

XX Treating condition associated with fetal alcohol syndrome in a subject

XX exposed to alcohol in utero or reducing neuronal death, involves

XX administering activity dependent neurotrophic factors I and/or III.

XX Disclosure; Page 51; 65pp; English.

XX The present invention relates to the treatment of a condition associated

XX with foetal alcohol syndrome (FAS), involving administering an activity

XX dependent neurotrophic factor (ADNF). ADNFs of the present invention may

XX also be used to treat neurological deficiencies and prevent neuronal cell

XX death. The present sequence is an ADNF peptide

XX Sequence 8 AA:

Query Match 33.9%; Score 41; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NBPVSIPQ 48
 |||||
 DB 1 NBPVSIPQ 8

RESULT 6
 AAB72322
 ID AAB72322 standard; peptide; 8 AA.

XX AAB72322;

DT 16-MAY-2001 (first entry)

XX Activity dependent neurotrophic factor III (ADNF III) peptide SEQ ID 2.

XX Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;

XX neuronal cell death; Alzheimer's disease; oxidative stress; VIP;

XX vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.

XX Synthetic.

```

XX  WO200112654-A2.
PN  22-FEB-2001.
XX  17-AUG-2000; 2000WO-US022861.
XX  18-AUG-1999; 99US-0149956P.
XX  (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX  Brennenman DE, Gozes I, Spong CY, Pinhasov A, Giladi E;
XX  WPI; 2001-202855/20.
XX  Novel Activity Dependent Neurotrophic Factor I useful for treating
PT  oxidative stress, reducing neuronal cell death and treating a condition
XX  associated with fetal alcohol syndrome.
XX  Claim 10; Page 57; 88pp; English.
XX  This invention relates to an activity dependent neurotrophic factor I
CC  (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72321 represent
CC  ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent
CC  ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical
CC  composition containing either ADNF I or ADNF III are useful for reducing
CC  neuronal cell death, e.g. death of spinal cord neurons, hippocampal
CC  neurons, cerebral cortical neurons and cholinergic neurons, in a patient
CC  infected with a virus, e.g. human immunodeficiency virus (HIV). The
CC  neuronal cell death is associated with excitotoxicity induced by N-
CC  methyl-D-aspartate (NMDA) stimulation, which is induced by beta-amyloid
CC  peptide in an Alzheimer's disease patient, or induced by cholinergic
CC  blockade. ADNF I, ADNF III and the pharmaceutical composition are also
CC  useful for treating oxidative stress in a patient, for reducing a
CC  condition, such as decreased body weight, decreased brain weight,
CC  decreased level of vasoreactive intestinal peptide (VIP) mRNA, and foetal
CC  death, associated with foetal alcohol syndrome
XX  SQ  Sequence 8 AA;

Query Match      33.9%; Score 41; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  41 NAFVSIQ 48
Db  1 NAFVSIQ 8

RESULT 7
AB07216
ID  ABB07216 standard; peptide; 8 AA.
XX
XX  ABB07216;
AC
XX
XX  26-MAR-2002 (first entry)
DT
XX
XX  ADNF III polypeptide active core site peptide sequence.
DE
XX
XX  ADNF; Activity Dependent Neurotrophic Factor; neurotrophic; neuroprotective;
KM  cerebroprotective; antidibetic; neuroleptic; anticonvulsant; anti-HIV;
KM  antiparkinsonian; tranquilizer; antialcoholic; vulnerary; antibacterial;
KM  antiinflammatory; antidote; ophthalmological; muscular; vasodilator;
XX  NMDA receptor.
XX
XX  Synthetic.
XX  OS
XX  WO200192333-A2.
XX  PN
XX  06-DEC-2001.
XX  PD
XX  31-MAY-2001; 2001WO-US017758.
XX  PF

```

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XX  31-MAY-2000; 2000US-0208944P.
PR  08-FEB-2001; 2001US-0267805P.
XX
XX  (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX  Spong CY, Brennenman D, Gozes I;
PI
XX  WPI; 2002-114330/15.
XX
XX  Use of an activity dependent neurotrophic factor for improving learning
PT  and/or memory in a subject by pre- or post-natal administration.
XX
XX  Claim 1; Page 51; 80pp; English.
XX
XX  The invention provides a method of improving learning and/or memory in a
CC  subject that involves administering pre- or postnatally an Activity
CC  Dependent Neurotrophic Factor (ADNF) to the subject. The ADNF polypeptide
CC  is an ADNF I and/or an ADNF III polypeptide comprising the core active
CC  site sequences ABB07215 or ABB07216. The method is useful for improving
CC  learning and/or memory in a subject; for treating a normal or old subject
CC  afflicted with neuropathology, Alzheimer's disease, Down's syndrome,
CC  normal mental capacity, mental retardation, for the treatment of central
CC  motor systems including degenerative conditions affecting the basal
CC  ganglia (see ABB07215 for a detailed description of the various
CC  conditions that can be treated by using the ADNF polypeptides). The
CC  present sequence represents the active core site sequence of the ADNF III
XX  polypeptide
XX  SQ  Sequence 8 AA;

Query Match      33.9%; Score 41; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  41 NAFVSIQ 48
Db  1 NAFVSIQ 8

RESULT 8
ABR39742
ID  ABR39742 standard; peptide; 8 AA.
XX
XX  ABR39742;
AC
XX
XX  23-JUN-2003 (first entry)
DT
XX
XX  ADNF I active core peptide fragment NAP.
DE
XX
XX  ADNF I; Activity Dependent Neurotrophic Factor I; neuroprotective;
KM  anti-HIV; neuroleptic; antiparkinsonian; neurotrophic; ADNF; NAP; SAL;
XX  Activity Dependent Neuroprotective Protein.
XX
XX  Unidentified.
XX  OS
XX  WO2003022226-A2.
XX  PN
XX  20-MAR-2003.
XX  PD
XX  12-SEP-2002; 2002WO-US029146.
XX  PF
XX  12-SEP-2001; 2001US-0322760P.
XX  PR  10-APR-2002; 2002US-0371961P.
XX
XX  (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX  Brennenman DE, Castellon R, Spong CY, Hauser JM, Gozes I;
XX  WPI; 2003-354501/33.
XX

```

PT New Activity Dependent Neurotrophic Factor I complex polypeptide, useful
PT for reducing neuronal cell death, treating oxidative stress in a patient,
PT or improving learning and/or memory in a subject with e.g. Alzheimer's
PT disease.
XX
XX
PS Disclosure; Page 2; 11pp; English.
XX
XX The invention relates to Activity Dependent Neurotrophic Factor I (ADNF
CC I) complex polypeptide selected from sequences ABR39744-754. The ADNF I
CC complex polypeptide is useful for reducing neuronal cell death in
CC conditions such as HIV infection, treating oxidative stress in a patient,
CC reducing a condition associated with fetal alcohol syndrome, or improving
CC learning and/or memory in a subject with e.g. Alzheimer's disease or
CC Down's syndrome. The ADNF complex polypeptides are also useful in
CC designing a drug treatment regime that can be individually tailored for
CC each patient affected by neurodegenerative disorders. The polypeptides
CC can also be used for diagnosing or treating Huntington's disease,
CC Wilson's disease, Parkinson's disease, AIDS-related dementia or
CC Tourette's syndrome. The present sequence represents a ADNF (activity
CC dependent neurotrophic protein) peptide, that has a biological
CC activity similar to a ADNF I peptide SAL
XX
SQ Sequence 8 AA;
Query Match 33.9%; Score 41; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 NAPSIPQ 48
Db 1 NAPSIPQ 8
RESULT 9
ADA07953
XX ADA07953 standard; peptide; 8 AA.
XX
AC ADA07953;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human activity dependent neuroprotective factor (ADNF) peptide #2.
XX
KM Human; glaucomatous optic neuropathy;
KM activity dependent neuroprotective factor; ADNF; ophthalmological.
XX
OS Homo sapiens.
XX
PN US2003166544-A1.
XX
PD 04-SEP-2003.
XX
PF 06-JUN-2002; 2002US-00164432.
XX
PR 07-SEP-2000; 2000US-0230964P.
PR 02-AUG-2001; 2001US-00921029.
XX
XX (CLAR/) CLARK A F.
PA (SHAD/) SHADE D L.
XX
XX Clark AF, Shade DL;
PI
XX WPI; 2003-720933/68.
XX
PT Treating glaucomatous optic neuropathy by administering a composition
PT comprising a peptide derived from or related to Activity Dependent
PT Neuroprotective Factor (ADNF).
XX
XX Claim 2; Page 2; 13pp; English.
XX
XX The present invention relates to a method for preventing and treating
CC glaucomatous optic neuropathy. The method comprises administering a
CC composition comprising a peptide derived from activity dependent

CC neuroprotective factor (ADNF). The method is useful for treating
CC glaucomatous optic neuropathy. The present sequence represents a peptide
CC from human ADNF.
XX
XX
SQ Sequence 8 AA;
Query Match 33.9%; Score 41; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 NAPSIPQ 48
Db 1 NAPSIPQ 8
RESULT 10
ADQ76121
ID ADQ76121 standard; peptide; 8 AA.
XX
AC ADQ76121;
XX
DT 07-OCT-2004 (first entry)
XX
DE ADNF III active core site peptide SEQ ID NO:2.
XX
XX activity dependent neurotrophic factor; ADNF; ADNF III; active core site;
KM immunosuppressive; nootropic; neuroprotective; antiinflammatory;
KM vasotrophic; muscular; CNS; thyromimetic; antithyroid; antihemetic;
KM antidiabetic; hepatotropic; vitruclide; dermatological; haemostatic;
KM autoimmune disease; multiple sclerosis; myasthenia gravis;
KM Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;
KM Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;
KM hypothyroiditis; primary biliary cirrhosis;
KM mixed connective tissue disease; chronic active hepatitis;
KM Graves' disease; hyperthyroiditis; scleroderma;
KM chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;
KM septic shock.
XX
OS Synthetic.
XX
XX WO2004060309-A2.
XX
XX 22-JUL-2004.
XX
PF 30-DEC-2003; 2003WO-US041540.
XX
PR 02-JAN-2003; 2003US-0437650P.
XX
XX (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Gozes I, Offen D, Giladi E, Melamed E, Breneman D;
PI
XX WPI; 2004-543782/52.
XX
XX Preventing or treating autoimmune diseases, such as multiple sclerosis,
PT rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic
PT shock, using an Activity Dependent Neurotrophic Factor (ADNF) polypeptide.
XX
XX Claim 1; SEQ ID NO 2; 39pp; English.
XX
XX The present invention describes a method for preventing or treating an
CC autoimmune disease in a subject. The method comprises administering an
CC activity dependent neurotrophic factor (ADNF) polypeptide, where the ADNF
CC polypeptide is a member selected from the group consisting of: (a) an
CC ADNF I polypeptide comprising an active core site with the amino acid
CC sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide
CC comprising an active core site with the amino acid sequence of SEQ ID
CC NO:2 (ADQ76121); and (c) a mixture of the ADNF I polypeptide of part (a)
CC and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
CC host cells, vectors and antibodies used in the methods are also disclosed
CC in the present invention. ADNF sequences have immunosuppressive,

CC neurotropic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
CC thymidimetic, antihypertoid, antirheumatic, antirheptic, hepatotropic,
CC virulent, dermatological, hemostatic, antidiabetic and antibacterial
CC activities, and can be used as neurotropic factor agonists. The methods
CC and compositions of the present invention are useful for the prevention
CC and/or treatment of autoimmune diseases, such as multiple sclerosis,
CC myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,
CC Behcet's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
CC disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
CC tissue disease, chronic active hepatitis, Graves'
CC disease/hypothyroiditis, scleroderma, chronic idiopathic
CC thrombocytopenic purpura, diabetic neuropathy and septic shock. The
CC present sequence represents an ADNP III active core site peptide from the
CC present invention.

```
Query Match      33.9%; Score 41; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	41	NAPVSI	PQ	48
Db	1	NAPVSI	PQ	8

```

RESULT 11
ADS73609
ID ADS73609 standard; peptide; 8 AA.

```

DT	16-DEC-2004	(first entry)
XX		
DE	ADNF III	active core site.

KM active core peptide; Activity Dependent Neurotrophic Factor; ADNF; ADNF-1; ADNF-1L; anxiety; depression; lipophilic moiety; penetration; activity; panic disorder; obsessive-compulsive disorder; post-traumatic stress disorder; social phobia; social anxiety disorder; specific phobia; generalized anxiety disorder; Major depression; dysthymia; bipolar disorder; NAP-cubulin; binding site; anxiolytic drug; neuroprotection.

OS Homo sapiens.

PN WO2004080957-A2.

PD 23-SEP-2004.

PF 11-MAR-2004; 2004WO-IL000232.

PR 12-MAR-2003; 2003US-0454505P.

PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.

PI Gozes I, Alcalay RN, Divinski I, Giladi E;

DR WPI; 2004-668930/65.

PT Treating or preventing anxiety or depression in a subject comprises

PT polypeptide to the subject.

PS Claim 2; SEQ ID NO 2; 46pp; English

This sequence represents the active core peptide derived from Activity Dependent Neurotrophic Factor (ADNF) III. This peptide may be used for treating or preventing anxiety or depression in a subject. This sequence may optionally be extended at either the N- and/or the C-terminals. The ADNF polypeptide of the invention may be encoded by a nucleic acid that is administered to the subject. It also contains a covalently bound lipophilic moiety to enhance penetration or activity. The subject suffers

from anxiety or depression and the ADNF polypeptide is administered to prevent anxiety or depression. The disease is selected from a panic disorder, obsessive-compulsive disorder, post-traumatic stress disorder, social phobia, social anxiety disorder, specific phobias, generalized anxiety disorder, major depression, dysrhythmia, and bipolar disorder. The ADNF polypeptide binds to the ADNF polypeptide binding site(s) and binds to the ADNF polypeptide binding site(s) is/are used to identify anxiolytic drugs and drugs that alleviate depression and provide neuroprotection.

SQ Sequence 8 AA:

Query Match	33.9%;	Score 41;	DB 8;	Length 8;
Best Local Similarity	100.0%;	Pred. No. 1.8e+06;		
Matches	8;	Conservative	0;	Mismatches
			0;	Gaps
				0;

QY	41	NAPVSIPQ	4
Db	1	NAPVSIPQ	8

RESULT 12
AAW64696
ID AAW64696 standard; protein; 10 AA

DT	17-OCT-2003	(revised)
DT	04-NOV-1998	(first entry)

DE Seq ID 33 from W09835042

KM Actively dependent neurotrophic factor III: ADNF-III; ADNP; cell death;
 KM activity dependent neuroprotective protein; neurone; excitotoxicity;
 KM spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;
 KM N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
 KM HIV infection.

OS unidentified

PN W09835042-A2

PD 13-AUG-1998.

PF 06-FEB-1998; 98WO-US002485.

PR 07-FEB-1997; 97US-0037404P.

PA (USSH) US SEC HEALTH & HUMAN SERVICES

PI Gozes I, Brenneman DE, Bassan M,

DR WPI; 1998-447239/38.

PT Activity dependent neurotrophic factor III polypeptide - useful therapeutically to prevent neuronal cell death associated with e.g. HIV infection, excitotoxicity or Alzheimer's disease.

PS Disclosure; Page; 121pp; English.

This specification describes the isolation of novel activity dependent
 neurotrophic factor III, ADNF-III (also known as activity dependent
 neuroprotective protein, ADNP) sequences. ADNF III polypeptides can be
 used to prevent neuronal cell death, of e.g. the spinal cord,
 hippocampal, cerebral cortical or cholinergic neurones associated with
 e.g. HIV infection, excitotoxicity induced by N-methyl-D-aspartate
 stimulation or beta-amyloid peptide in Alzheimer's disease. The
 polypeptides can also be combined with a carrier to alleviate learning
 impairment produced by cholinergic blockage in Alzheimer's patients. The
 nucleic acids are useful in polypeptide production and to detect ADNF III
 polynucleotide in biological samples, while the antibodies are useful
 therapeutically and to isolate ADNF III polypeptides. NOTE: This sequence
 does not appear in the specification but is present in the sequence ID
 listing. (Updated on 17-OCT-2003 to standardise OS field)

SQ Sequence 10 AA;
 Query Match 33.9%; Score 41; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.32;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 NAFVSIPQ 48
 |||||
 3 NAFVSIPQ 10

RESULT 13
 AAY71139
 ID AAY71139 standard; peptide; 10 AA.
 XX
 AC AAY71139;
 XX
 DT 08-SEP-2000 (first entry)
 XX
 DE Human Activity Dependent Neurotrophic Factor (ADNF) III generic peptide.
 XX
 KW Activity Dependent Neurotrophic Factor III; ADNF; human; ADNF;
 KW Activity Dependent Neuroprotective Protein; chromosome 20q13.2; ADNFLE;
 KW autosomal dominant nocturnal frontal-lobe epilepsy; neuronal cell death;
 KW neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;
 KW Alzheimer's disease; beta-amyloid peptide; Huntington's disease;
 KW epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;
 KW amyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;
 KW mitochondrial abnormality; Wernicke's encephalopathy; homocysteinuria;
 KW hyperproliferation; sulphite oxide disease; Tourette's syndrome; noctropic;
 KW Down's syndrome; drug addiction; developmental retardation; antileptic;
 KW learning impairment; anticonvulsant; neuroprotective; anti-HIV.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Xaa= (R1)x= N-terminal amino acid sequence
 FT Misc-difference 10 comprising 1-40 residues, where x= one or zero"
 FT Misc-difference 10 /note= "Xaa= (R2)y= C-terminal amino acid sequence
 FT Misc-difference 10 comprising 1-40 residues, where y= one or zero"
 XX
 PN WO200027875-A2.
 PD 18-MAY-2000.
 XX
 PF 04-NOV-1999; 99WO-US026213.
 XX
 PR 06-NOV-1998; 98US-00187310.
 XX
 PA (USAS) GOVERNMENT US REPRESENT AS.
 PA (UTRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 XX
 PI Gozes I, Breneman DE, Bassan M, Zamostiano R;
 XX
 DR WPI; 2000-376491/32.
 XX
 PT New nucleic acid encoding an activity dependent neurotrophic factor III
 PT (ADNF III) useful in the treatment of neurological deficiencies and for
 PT preventing neuronal cell death.
 XX
 PS Claim 25; Page 95; 136pp; English.
 XX
 CC The present sequence is the human Activity Dependent Neurotrophic Factor
 CC (ADNF) III generic peptide. It consists of the ADNF III-8 or NAF peptide,
 CC flanked by N- and C-terminal generic sites, comprising 1-40 amino acids.
 CC ADNF III is also called an Activity Dependent Neuroprotective Protein
 CC (ADNP). The human gene was mapped to chromosome 20q13.2 and is linked to
 CC autosomal dominant nocturnal frontal-lobe epilepsy (ADNFLE) gene. It is
 CC expressed in the astrocytes, brain and also in foetal lung and endocrine
 CC tissues. This sequence has homology to ADNF I and hepo0, heat shock
 CC protein and Pifl, a DNA repair protein. The ADNF III polypeptides are

CC useful for the treatment of neurological deficiencies and for prevention
 CC of neuronal cell death associated with gp120, the envelope protein from
 CC HIV; N-methyl-D-Aspartic acid (excito-toxicity); tetrodotoxin (blockage
 CC of electrical activity); and beta-amyloid peptide, a substance related to
 CC neuronal degeneration in Alzheimer's disease. It is useful for the
 CC treatment of Huntington's disease, AIDS dementia complex, epilepsy,
 CC neuropathic pain syndromes, Parkinson's disease, amyotrophic lateral
 CC sclerosis (ALS), mitochondrial abnormalities, Leber's disease, Wernicke's
 CC encephalopathy, Alzheimer's disease, homocysteinuria, hyperproliferation,
 CC sulphite oxide disease, Tourette's syndrome, oxidative stress induced
 CC neuronal death, Down's syndrome, developmental retardation and learning
 CC impairments, drug addiction, tolerance and dependency
 XX

SQ Sequence 10 AA;
 Query Match 33.9%; Score 41; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.32;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 NAFVSIPQ 48
 |||||
 2 NAFVSIPQ 9

RESULT 14
 AAB23488
 ID AAB23488 standard; peptide; 10 AA.
 XX
 AC AAB23488;
 XX
 DT 14-MAY-2003 (revised)
 DT 22-JAN-2001 (first entry)
 XX
 DE Activity dependent neurotrophic factor III peptide #1.
 XX
 KW Activity dependent neurotrophic factor; ADNF; FAS;
 KW foetal alcohol syndrome; gene therapy; neurological deficiency;
 KW neuronal cell death.
 XX
 OS Unidentified.
 XX
 PN WO200053217-A2.
 PD 14-SEP-2000.
 XX
 PF 10-MAR-2000; 2000WO-US006364.
 XX
 PR 12-MAR-1999; 99US-00267511.
 XX
 PA (UTRA-) UNIV RAMOT.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Breneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;
 XX
 DR WPI; 2000-601940/57.
 XX
 PT Treating condition associated with fetal alcohol syndrome in a subject
 PT exposed to alcohol in utero or reducing neuronal death, involves
 PT administering activity dependent neurotrophic factors I and/or III.
 XX
 PS Claim 10; Page 4; 65pp; English.
 XX
 CC The present invention relates to the treatment of a condition associated
 CC with foetal alcohol syndrome (FAS), involving administering an activity
 CC dependent neurotrophic factor (ADNF). ADNFs of the present invention may
 CC also be used to treat neurological deficiencies and prevent neuronal cell
 CC death. The present sequence is an ADNF peptide. (Updated on 14-MAY-2003
 CC to correct PS field.)
 XX

SQ Sequence 10 AA;
 Query Match 33.9%; Score 41; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.32;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Job time : 119.825 secs

QY 41 NAPVSIPO 48
 |||||
 Db 3 NAPVSIPO 10

RESULT 15
 AAB72323
 ID AAB72323 standard; peptide; 10 AA.

XX AAB72323;

XX 16-MAY-2001 (first entry)

DE Activity dependent neurotrophic factor III (ADNF III) peptide SEQ ID 17.

KM Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;

KM neuronal cell death; Alzheimer's disease; oxidative stress; VIP;

KM vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.

OS Synthetic.

XX WO200112654-A2.

XX 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022861.

PR 18-AUG-1999; 99US-0149956P.

PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

PI (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Breneman DE, Gozes I, Spong CY, Pinhasov A, Giladi E;

PT Novel Activity Dependent Neurotrophic Factor I useful for treating

PS Claim 16; Page 57; 88pp; English.

CC This invention relates to an activity dependent neurotrophic factor I

CC (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72321 represent

CC ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent

CC ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical

CC composition containing either ADNF I or ADNF III are useful for reducing

CC neuronal cell death, e.g. death of spinal cord neurons, hippocampal

CC neurons, cerebral cortical neurons and cholinergic neurons, in a patient

CC infected with a virus, e.g. human immunodeficiency virus (HIV). The

CC neuronal cell death is associated with excitotoxicity induced by N-

CC methyl-D-aspartate (NMDA) stimulation, which is induced by beta-amyloid

CC peptide in an Alzheimer's disease patient, or induced by cholinergic

CC blockade. ADNF I, ADNF III and the pharmaceutical composition are also

CC useful for treating oxidative stress in a patient, for reducing a

CC condition, such as decreased body weight, decreased brain weight,

CC decreased level of vasoactive intestinal peptide (VIP) mRNA, and foetal

CC death, associated with foetal alcohol syndrome

XX SQ Sequence 10 AA;

Query Match 33.9%; Score 41; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.32; Mismatches 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 41 NAPVSIPO 48
 |||||
 Db 3 NAPVSIPO 10

Search completed: February 23, 2005, 19:30:08


```
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-291200US
CURRENT APPLICATION NUMBER: US/09/187,330
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/037,404
EARLIER FILING DATE: 1997-02-07
EARLIER APPLICATION NUMBER: WO PCT/US98/02485
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III
US-09-187-330-33
```

```
Query Match      33.9%; Score 41; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      41 NAFVSIPQ 48
         |||||
Db       3 NAFVSIPQ 10
```

```
RESULT 3
US-09-187-330-34
Sequence 34, Application US/09187330
Patent No. 6613740
GENERAL INFORMATION:
APPLICANT: Gozes, Iliana
APPLICANT: Brenneman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamosciano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-291200US
CURRENT APPLICATION NUMBER: US/09/187,330
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/037,404
EARLIER FILING DATE: 1997-02-07
EARLIER APPLICATION NUMBER: WO PCT/US98/02485
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III
US-09-187-330-34
```

```
Query Match      33.9%; Score 41; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      41 NAFVSIPQ 48
         |||||
Db       4 NAFVSIPQ 11
```

```
RESULT 4
US-09-187-330-35
Sequence 35, Application US/09187330
```

```
Patent No. 6613740
GENERAL INFORMATION:
APPLICANT: Gozes, Iliana
APPLICANT: Brenneman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamosciano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-291200US
CURRENT APPLICATION NUMBER: US/09/187,330
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/037,404
EARLIER FILING DATE: 1997-02-07
EARLIER APPLICATION NUMBER: WO PCT/US98/02485
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III
US-09-187-330-35
```

```
Query Match      33.9%; Score 41; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      41 NAFVSIPQ 48
         |||||
Db       6 NAFVSIPQ 13
```

```
RESULT 5
US-09-187-330-12
Sequence 12, Application US/09187330
Patent No. 6613740
GENERAL INFORMATION:
APPLICANT: Gozes, Iliana
APPLICANT: Brenneman, Douglas E.
APPLICANT: Bassan, Merav
APPLICANT: Zamosciano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-291200US
CURRENT APPLICATION NUMBER: US/09/187,330
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/037,404
EARLIER FILING DATE: 1997-02-07
EARLIER APPLICATION NUMBER: WO PCT/US98/02485
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III
US-09-187-330-12
```

```
Query Match      33.9%; Score 41; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      41 NAFVSIPQ 48
```


Db 9 NAPVSIQ 16

RESULT 6

US-09-187-330-10
 ; Sequence 10, Application US/09187330
 ; Patent No. 6613740
 ; GENERAL INFORMATION:
 ; APPLICANT: Gozes, Iliana
 ; APPLICANT: Breneman, Douglas E.
 ; APPLICANT: Baasan, Merav
 ; APPLICANT: Zamostiano, Rachel
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by the Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
 ; FILE REFERENCE: 015280-291200US
 ; CURRENT APPLICATION NUMBER: US/09/187,330
 ; CURRENT FILING DATE: 1998-11-06
 ; EARLIER APPLICATION NUMBER: US 60/037,404
 ; EARLIER FILING DATE: 1997-02-07
 ; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
 ; EARLIER FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 88
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:activity
 ; OTHER INFORMATION: dependent neurotrophic factor III (ADNF III)
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)..(40)
 ; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-40 may be
 ; OTHER INFORMATION: present or absent
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (49)..(88)
 ; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 49-88 may be
 ; OTHER INFORMATION: present or absent
 ; US-09-187-330-10

Query Match 33.9%; Score 41; DB 4; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAPVSIQ 48
 Db 41 NAPVSIQ 48

RESULT 7

US-09-187-330-57
 ; Sequence 57, Application US/09187330
 ; Patent No. 6613740
 ; GENERAL INFORMATION:
 ; APPLICANT: Gozes, Iliana
 ; APPLICANT: Breneman, Douglas E.
 ; APPLICANT: Baasan, Merav
 ; APPLICANT: Zamostiano, Rachel
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by the Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
 ; FILE REFERENCE: 015280-291200US
 ; CURRENT APPLICATION NUMBER: US/09/187,330
 ; CURRENT FILING DATE: 1998-11-06
 ; EARLIER APPLICATION NUMBER: US 60/037,404
 ; EARLIER FILING DATE: 1997-02-07

; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
 ; EARLIER FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 57
 ; LENGTH: 726
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-187-330-57

Query Match 33.9%; Score 41; DB 4; Length 726;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAPVSIQ 48
 Db 59 NAPVSIQ 66

RESULT 8

US-09-187-330-32
 ; Sequence 32, Application US/09187330
 ; Patent No. 6613740
 ; GENERAL INFORMATION:
 ; APPLICANT: Gozes, Iliana
 ; APPLICANT: Breneman, Douglas E.
 ; APPLICANT: Baasan, Merav
 ; APPLICANT: Zamostiano, Rachel
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by the Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
 ; FILE REFERENCE: 015280-291200US
 ; CURRENT APPLICATION NUMBER: US/09/187,330
 ; CURRENT FILING DATE: 1998-11-06
 ; EARLIER APPLICATION NUMBER: US 60/037,404
 ; EARLIER FILING DATE: 1997-02-07
 ; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
 ; EARLIER FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 32
 ; LENGTH: 781
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human activity dependent neurotrophic factor III
 ; OTHER INFORMATION: (ADNF III)
 ; US-09-187-330-32

Query Match 33.9%; Score 41; DB 4; Length 781;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAPVSIQ 48
 Db 33 NAPVSIQ 40

RESULT 9

US-09-187-330-31
 ; Sequence 31, Application US/09187330
 ; Patent No. 6613740
 ; GENERAL INFORMATION:
 ; APPLICANT: Gozes, Iliana
 ; APPLICANT: Breneman, Douglas E.
 ; APPLICANT: Baasan, Merav
 ; APPLICANT: Zamostiano, Rachel
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by the Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
 ; FILE REFERENCE: 015280-291200US

```
/ CURRENT APPLICATION NUMBER: US/09/187,330
/ CURRENT FILING DATE: 1998-11-06
/ EARLIER APPLICATION NUMBER: US 60/037,404
/ EARLIER FILING DATE: 1997-02-07
/ EARLIER APPLICATION NUMBER: WO PCT/US98/02485
/ EARLIER FILING DATE: 1998-02-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 31
/ LENGTH: 787
/ TYPE: PRT
/ ORGANISM: Mus musculus
/ FEATURE:
/ OTHER INFORMATION: mouse activity dependent neurotrophic factor III
/ OTHER INFORMATION: (ADNF III)
US-09-187-330-31
```

```
Query Match          33.9%; Score 41; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 41 NAPVISIPQ 48
Db 33 NAPVISIPQ 40
```

```
RESULT 10
US-09-187-330-41
/ Sequence 41, Application US/09187330
/ Patent No. 6613740
/ GENERAL INFORMATION:
/ APPLICANT: Gozes, Iilana
/ APPLICANT: Breneman, Douglas E.
/ APPLICANT: Bassan, Merav
/ APPLICANT: Zamoshtano, Rachel
/ APPLICANT: The Government of the United States of America
/ APPLICANT: as represented by the Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
/ FILE REFERENCE: 015280-291200US
/ CURRENT APPLICATION NUMBER: US/09/187,330
/ CURRENT FILING DATE: 1998-11-06
/ EARLIER APPLICATION NUMBER: US 60/037,404
/ EARLIER FILING DATE: 1997-02-07
/ EARLIER APPLICATION NUMBER: WO PCT/US98/02485
/ EARLIER FILING DATE: 1998-02-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 41
/ LENGTH: 800
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(800)
/ OTHER INFORMATION: translation of H3' human ADNF III cDNA clone
US-09-187-330-41
```

```
Query Match          33.9%; Score 41; DB 4; Length 800;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 41 NAPVISIPQ 48
Db 52 NAPVISIPQ 59
```

```
RESULT 11
US-09-187-330-3
/ Sequence 3, Application US/09187330
/ Patent No. 6613740
/ GENERAL INFORMATION:
/ APPLICANT: Gozes, Iilana
```

```
/ APPLICANT: Breneman, Douglas E.
/ APPLICANT: Bassan, Merav
/ APPLICANT: Zamoshtano, Rachel
/ APPLICANT: The Government of the United States of America
/ APPLICANT: as represented by the Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
/ FILE REFERENCE: 015280-291200US
/ CURRENT APPLICATION NUMBER: US/09/187,330
/ CURRENT FILING DATE: 1998-11-06
/ EARLIER APPLICATION NUMBER: US 60/037,404
/ EARLIER FILING DATE: 1997-02-07
/ EARLIER APPLICATION NUMBER: WO PCT/US98/02485
/ EARLIER FILING DATE: 1998-02-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 806
/ TYPE: PRT
/ ORGANISM: Mus musculus
/ FEATURE:
/ OTHER INFORMATION: mouse activity dependent neurotrophic factor III
/ OTHER INFORMATION: (ADNF III) cDNA clone
US-09-187-330-3
```

```
Query Match          33.9%; Score 41; DB 4; Length 806;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 41 NAPVISIPQ 48
Db 52 NAPVISIPQ 59
```

```
RESULT 12
US-09-187-330-55
/ Sequence 55, Application US/09187330
/ Patent No. 6613740
/ GENERAL INFORMATION:
/ APPLICANT: Gozes, Iilana
/ APPLICANT: Breneman, Douglas E.
/ APPLICANT: Bassan, Merav
/ APPLICANT: Zamoshtano, Rachel
/ APPLICANT: The Government of the United States of America
/ APPLICANT: as represented by the Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
/ FILE REFERENCE: 015280-291200US
/ CURRENT APPLICATION NUMBER: US/09/187,330
/ CURRENT FILING DATE: 1998-11-06
/ EARLIER APPLICATION NUMBER: US 60/037,404
/ EARLIER FILING DATE: 1997-02-07
/ EARLIER APPLICATION NUMBER: WO PCT/US98/02485
/ EARLIER FILING DATE: 1998-02-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 55
/ LENGTH: 828
/ TYPE: PRT
/ ORGANISM: Mus musculus
/ OTHER INFORMATION:
US-09-187-330-55
```

```
Query Match          33.9%; Score 41; DB 4; Length 828;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 41 NAPVISIPQ 48
Db 74 NAPVISIPQ 81
```

```
RESULT 13
US-09-187-330-59
```

```
/ Sequence 59, Application US/09187330
/ Patent No. 6613740
/ GENERAL INFORMATION:
/ APPLICANT: Gozes, Illana
/ APPLICANT: Brenneman, Douglas E.
/ APPLICANT: Bassan, Merav
/ APPLICANT: Zamosciano, Rachel
/ APPLICANT: The Government of the United States of America
/ APPLICANT: as represented by the Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
/ FILE REFERENCE: 015280-291200US
/ CURRENT APPLICATION NUMBER: US/09/187,330
/ EARLIER FILING DATE: 1998-11-06
/ EARLIER APPLICATION NUMBER: US 60/037,404
/ EARLIER FILING DATE: 1997-02-07
/ EARLIER APPLICATION NUMBER: WO PCT/US98/02485
/ EARLIER FILING DATE: 1998-02-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 59
/ LENGTH: 874
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-187-330-59
```

```
Query Match      33.9%; Score 41; DB 4; Length 874;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      41 NAFVSIQ 48
Db      126 NAFVSIQ 133
```

```
RESULT 14
US-09-187-330-1
/ Sequence 1, Application US/09187330
/ Patent No. 6613740
/ GENERAL INFORMATION:
/ APPLICANT: Gozes, Illana
/ APPLICANT: Brenneman, Douglas E.
/ APPLICANT: Bassan, Merav
/ APPLICANT: Zamosciano, Rachel
/ APPLICANT: The Government of the United States of America
/ APPLICANT: as represented by the Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
/ FILE REFERENCE: 015280-291200US
/ CURRENT APPLICATION NUMBER: US/09/187,330
/ EARLIER FILING DATE: 1998-11-06
/ EARLIER APPLICATION NUMBER: US 60/037,404
/ EARLIER FILING DATE: 1997-02-07
/ EARLIER APPLICATION NUMBER: WO PCT/US98/02485
/ EARLIER FILING DATE: 1998-02-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 1000
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: H3' human activity dependent neurotrophic factor
/ OTHER INFORMATION: III (ADNF III) clone
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (801)
/ OTHER INFORMATION: Xaa = unknown
/ NAME/KEY: MOD_RES
/ LOCATION: (817)
/ OTHER INFORMATION: Xaa = unknown
/ FEATURE:
```

```
/ NAME/KEY: MOD_RES
/ LOCATION: (821)
/ OTHER INFORMATION: Xaa = unknown
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (833)
/ OTHER INFORMATION: Xaa = unknown
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (854)
/ OTHER INFORMATION: Xaa = unknown
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (866)
/ OTHER INFORMATION: Xaa = unknown
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (870)
/ OTHER INFORMATION: Xaa = unknown
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (877)
/ OTHER INFORMATION: Xaa = unknown
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (882)
/ OTHER INFORMATION: Xaa = unknown
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (922)
/ OTHER INFORMATION: Xaa = unknown
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (948)
/ OTHER INFORMATION: Xaa = unknown
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (959)
/ OTHER INFORMATION: Xaa = unknown
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (964)
/ OTHER INFORMATION: Xaa = unknown
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (967)
/ OTHER INFORMATION: Xaa = unknown
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (980)
/ OTHER INFORMATION: Xaa = unknown
/ US-09-187-330-1

Query Match      33.9%; Score 41; DB 4; Length 1000;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      41 NAFVSIQ 48
Db      52 NAFVSIQ 59

RESULT 15
US-09-364-609-8
/ Sequence 8, Application US/09364609A
/ Patent No. 6649411
/ GENERAL INFORMATION:
/ APPLICANT: Gozes, Illana
/ APPLICANT: Brenneman, Douglas E.
/ APPLICANT: Zamosciano, Rachel
/ APPLICANT: Gelber, Edgar
/ APPLICANT: Pinhasov, Albert
/ APPLICANT: Bassan, Merav
```

```

; APPLICANT: Ramot University Authority for Applied Research &
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Methods of Inhibiting Cancer Cells with ADNF III
; TITLE OF INVENTION: Antisense Oligonucleotides
; FILE REFERENCE: 019856-000100US
; CURRENT APPLICATION NUMBER: US/09/364,609A
; CURRENT FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human activity dependent neurotrophic factor III
; OTHER INFORMATION: (ADNF III) cDNA
US-09-364-609-8

```

```

Query Match          33.9%; Score 41; DB 4; Length 1102;
Best Local Similarity 100.0%; Pred.No.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      41  NAPVSIPQ 48
        |||||
Db      354  NAPVSIPQ 361

```

Search completed: February 23, 2005, 19:36:17
Job time : 38.8305 secs

Query Match	33.9%	Score 41;	DB 9;	Length 8;
Best Local Similarity	100.0%	Pred. No. 1.2e+06;		
Matches	8;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY 41 NAPVSIPO 48
Db 1 NAPVSIPO 8

RESULT 2

US-10-164-432-4
; Sequence 4, Application US/10164432
; Publication No. US2003016544A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Inc.
; APPLICANT: Clark, Abbot F.
; APPLICANT: Debra, Shade L.
; TITLE OF INVENTION: The Use of ADNP for the Treatment of Glaucomatous Optic Neuropath
; FILE REFERENCE: 1975A US
; CURRENT APPLICATION NUMBER: US/10/164,432
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/921,029
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/230,964
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-164-432-4

Query Match 33.9%; Score 41; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAPVSIPO 48
Db 1 NAPVSIPO 8

RESULT 3

US-10-296-849-2
; Sequence 2, Application US/10296849
; Publication No. US20040048801A1
; GENERAL INFORMATION:
; APPLICANT: Spang, Catherine Y.
; APPLICANT: Breneman, Douglas
; APPLICANT: Gozes, Iilana
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied and
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Use of ADNP for Enhancing Learning and Memory
; FILE REFERENCE: 15280W-004200US
; CURRENT APPLICATION NUMBER: US/10/296,849
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/208,944
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 60/267,805
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: WO PCT/US01/17758
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence:Activity
; OTHER INFORMATION: Dependent Neurotrophic Factor III (ADNF III)
; OTHER INFORMATION: active core site, NMP or ADNF III-8
US-10-296-849-2

Query Match 33.9%; Score 41; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAPVSIPO 48
Db 1 NAPVSIPO 8

RESULT 4

US-10-623-272-6
; Sequence 6, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Iilana
; APPLICANT: Breneman, Douglas E.
; APPLICANT: Basan, Merav
; APPLICANT: Zamoshtiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence:ADNF III-8
; OTHER INFORMATION: active site core peptide, clone 25 sequence (NAP)
US-10-623-272-6

Query Match 33.9%; Score 41; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAPVSIPO 48
Db 1 NAPVSIPO 8

RESULT 5

US-09-267-511-23
; Sequence 23, Application US/09267511
; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Breneman, Douglas E.
; APPLICANT: Spang, Catherine Y.
; APPLICANT: Gozes, Iilana
; APPLICANT: Basan, Merav
; APPLICANT: Zamoshtiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 23
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III
US-09-267-511-23

Query Match 33.9%; Score 41; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIPO 48
Db 3 NAFVSIPO 10

RESULT 6
US-10-296-849-20

Sequence 20, Application US/10296849
Publication No. US20040048801A1
GENERAL INFORMATION:
APPLICANT: Spong, Catherine Y.
APPLICANT: Breneman, Douglas
APPLICANT: Gozes, Iilana
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied and
Industrial Development, Ltd.
TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
FILE REFERENCE: 15280W-004200US
CURRENT APPLICATION NUMBER: US/10/296,849
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/208,944
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: US 60/267,805
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: WO PCT/US01/17758
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III
US-10-296-849-20

Query Match 33.9%; Score 41; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIPO 48
Db 3 NAFVSIPO 10

RESULT 7
US-10-623-272-33

Sequence 33, Application US/10623272
Publication No. US20040053313A1
GENERAL INFORMATION:
APPLICANT: Gozes, Iilana
APPLICANT: Breneman, Douglas E.
APPLICANT: Basan, Merav
APPLICANT: Zamostiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
Department of Health and Human Services

TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
FILE REFERENCE: 015280-291200US
CURRENT APPLICATION NUMBER: US/10/623,272
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III
US-10-623-272-33

Query Match 33.9%; Score 41; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIPO 48
Db 3 NAFVSIPO 10

RESULT 8
US-09-267-511-24

Sequence 24, Application US/09267511
Patent No. US2002011301A1
GENERAL INFORMATION:
APPLICANT: Breneman, Douglas E.
APPLICANT: Spong, Catherine Y.
APPLICANT: Gozes, Iilana
APPLICANT: Basan, Merav
APPLICANT: Zamostiano, Rachel
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
Department of Health and Human Services
APPLICANT: Ramot University Authority for Applied Research
and Industrial Development, Ltd.
TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
Death with ADNF Polypeptides
FILE REFERENCE: 015280-377000US
CURRENT APPLICATION NUMBER: US/09/267,511
CURRENT FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:ADNF III
US-09-267-511-24

Query Match 33.9%; Score 41; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIPO 48
Db 4 NAFVSIPO 11

RESULT 9
US-10-296-849-21

Sequence 21, Application US/10296849

```
/ Publication No. US20040048801A1
/ GENERAL INFORMATION:
/ APPLICANT: Spong, Catherine Y.
/ APPLICANT: Brennenman, Douglas
/ APPLICANT: Gozes, Iliana
/ APPLICANT: The Government of the United States of America
/ APPLICANT: as represented by the Secretary of the
/ APPLICANT: Department of Health and Human Services
/ APPLICANT: Ramot University Authority for Applied and
/ APPLICANT: Industrial Development, Ltd.
/ TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
/ FILE REFERENCE: 15280W-004200US
/ CURRENT APPLICATION NUMBER: US/10/296,849
/ CURRENT FILING DATE: 2003-06-18
/ PRIOR APPLICATION NUMBER: US 60/208,944
/ PRIOR FILING DATE: 2000-05-31
/ PRIOR APPLICATION NUMBER: US 60/267,805
/ PRIOR FILING DATE: 2001-02-08
/ PRIOR APPLICATION NUMBER: WO PCT/US01/17758
/ PRIOR FILING DATE: 2001-05-31
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 21
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:ADNF III
/ OTHER INFORMATION: polypeptide
US-10-296-849-21
```

```
Query Match      33.9%; Score 41; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      41 NAPSIPQ 48
         |||||
Db       4 NAPSIPQ 11
```

```
RESULT 10
US-10-623-272-34
/ Sequence 34, Application US/10623272
/ Publication No. US20040053131A1
/ GENERAL INFORMATION:
/ APPLICANT: Gozes, Iliana
/ APPLICANT: Brennenman, Douglas E.
/ APPLICANT: Bassan, Merav
/ APPLICANT: Zamostiano, Rachel
/ APPLICANT: The Government of the United States of America
/ APPLICANT: as represented by the Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Actively Dependent Neurotrophic Factor III (ADNF III)
/ FILE REFERENCE: 015280-291200US
/ CURRENT APPLICATION NUMBER: US/10/623,272
/ CURRENT FILING DATE: 2003-07-17
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 34
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:ADNF III
/ OTHER INFORMATION: polypeptide
US-10-623-272-34
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```
Query Match      33.9%; Score 41; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      41 NAPSIPQ 48
         |||||
Db       4 NAPSIPQ 11
```

```
RESULT 11
US-09-267-511-25
/ Sequence 25, Application US/09267511
/ Patent No. US2002011301A1
/ GENERAL INFORMATION:
/ APPLICANT: Brennenman, Douglas E.
/ APPLICANT: Spong, Catherine Y.
/ APPLICANT: Gozes, Iliana
/ APPLICANT: Bassan, Merav
/ APPLICANT: Zamostiano, Rachel
/ APPLICANT: The Government of the United States of America
/ APPLICANT: as represented by the Secretary of the
/ APPLICANT: Department of Health and Human Services
/ APPLICANT: Ramot University Authority for Applied Research
/ TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
/ TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
/ FILE REFERENCE: 015280-377000US
/ CURRENT APPLICATION NUMBER: US/09/267,511
/ CURRENT FILING DATE: 1999-03-12
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 25
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:ADNF III
/ OTHER INFORMATION: polypeptide
US-09-267-511-25
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```
Query Match      33.9%; Score 41; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      41 NAPSIPQ 48
         |||||
Db       6 NAPSIPQ 13
```

```
RESULT 12
US-10-296-849-22
/ Sequence 22, Application US/10296849
/ Publication No. US20040048801A1
/ GENERAL INFORMATION:
/ APPLICANT: Spong, Catherine Y.
/ APPLICANT: Brennenman, Douglas
/ APPLICANT: Gozes, Iliana
/ APPLICANT: The Government of the United States of America
/ APPLICANT: as represented by the Secretary of the
/ APPLICANT: Department of Health and Human Services
/ APPLICANT: Ramot University Authority for Applied and
/ APPLICANT: Industrial Development, Ltd.
/ TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
/ FILE REFERENCE: 15280W-004200US
/ CURRENT APPLICATION NUMBER: US/10/296,849
/ CURRENT FILING DATE: 2003-06-18
/ PRIOR APPLICATION NUMBER: US 60/208,944
/ PRIOR FILING DATE: 2000-05-31
/ PRIOR APPLICATION NUMBER: US 60/267,805
/ PRIOR FILING DATE: 2001-02-08
/ PRIOR APPLICATION NUMBER: WO PCT/US01/17758
/ PRIOR FILING DATE: 2001-05-31
/ NUMBER OF SEQ ID NOS: 23
```



```

; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; US-10-296-849-22

```

```

Query Match      33.9%; Score 41; DB 15; Length 15;
Best Local Similarity 100.0%; Pred.No. 0.52;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      41 NAFVSIPO 48
        |||||
Db      6 NAFVSIPO 13

```

```

RESULT 13
US-10-623-272-35
; Sequence 35, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Iliana
; APPLICANT: Breneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamosciano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; US-10-623-272-35

```

```

Query Match      33.9%; Score 41; DB 15; Length 15;
Best Local Similarity 100.0%; Pred.No. 0.52;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      41 NAFVSIPO 48
        |||||
Db      6 NAFVSIPO 13

```

```

RESULT 14
US-09-267-511-19
; Sequence 19, Application US/09267511
; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Breneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Iliana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamosciano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the

```

```

; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: Ramot Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; US-09-267-511-19

```

```

Query Match      33.9%; Score 41; DB 9; Length 17;
Best Local Similarity 100.0%; Pred.No. 0.59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      41 NAFVSIPO 48
        |||||
Db      6 NAFVSIPO 13

```

```

RESULT 15
US-09-267-511-26
; Sequence 26, Application US/09267511
; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Breneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Iliana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamosciano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; US-09-267-511-26

```

```

Query Match      33.9%; Score 41; DB 9; Length 17;
Best Local Similarity 100.0%; Pred.No. 0.59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      41 NAFVSIPO 48
        |||||
Db      8 NAFVSIPO 15

```

Search completed: February 23, 2005, 19:51:27
Job time : 88 secs

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OM protein - protein search, using sw model

Run on: February 23, 2005, 19:09:56 ; Search time 114.35 Seconds
(without alignments)
394.078 Million cell updates/sec

Title: US-09-267-511-4
Perfect score: 121
Sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXXXX 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	33.9	823	1 ADNP_RAT	Q9JK18 ratu
2	41	33.9	828	1 ADNP_MOUSE	Q9Z103 mus
3	41	33.9	1089	2 Q6Z047	Q6Z047 mus
4	41	33.9	1102	1 ADNP_HUMAN	Q9H280 hom
5	41	33.9	1102	2 Q6DHZ8	Q6DHZ8 hom
6	36	29.8	445	2 Q6C9B5	Q6C9B5 yar
7	36	29.8	470	2 Q82YV3	Q82YV3 yar
8	36	29.8	481	2 Q8E338	Q8E338 yar
9	36	29.8	510	2 Q8P023	Q8P023 yar
10	36	29.8	510	2 Q99ZK7	Q99ZK7 yar
11	36	29.8	510	2 Q8K7F1	Q8K7F1 yar
12	36	29.8	511	2 Q8DUC1	Q8DUC1 yar
13	36	29.8	631	2 Q912G3	Q912G3 yar
14	36	29.8	1396	2 Q6KAS0	Q6KAS0 yar
15	36	29.8	1502	1 GEM5_MOUSE	GEM5_MOUSE
16	35	28.9	189	2 Q8SZD3	Q8SZD3 yar
17	35	28.9	189	2 Q9V7Z8	Q9V7Z8 yar
18	35	28.9	299	2 Q92XPO	Q92XPO yar
19	35	28.9	3415	2 Q9XCF3	Q9XCF3 yar
20	35	28.9	4027	2 Q740V0	Q740V0 yar
21	34	28.1	136	2 Q28744	Q28744 yar
22	34	28.1	158	2 Q8BGB7	Q8BGB7 yar
23	34	28.1	464	2 Q6FFK0	Q6FFK0 yar
24	34	28.1	503	2 Q84LK3	Q84LK3 yar
25	34	28.1	505	2 Q9V3B2	Q9V3B2 yar
26	34	28.1	597	2 Q6MAF9	Q6MAF9 yar
27	34	28.1	1272	1 FMR2_MOUSE	FMR2_MOUSE
28	34	28.1	1272	1 FMR2_PANTR	FMR2_PANTR
29	34	28.1	1272	1 FMR2_PONPY	FMR2_PONPY
30	34	28.1	1272	2 Q72400	Q72400 yar
31	34	28.1	1311	1 FMR2_HUMAN	FMR2_HUMAN

32	34	28.1	1789	2 Q8T145	Q8T145 dictyosteli
33	33	27.3	104	2 Q8A044	Q8A044 bacteroides
34	33	27.3	197	1 WRBA_SALTI	WRBA_SALTI salmonella
35	33	27.3	197	1 WRBA_SALTY	WRBA_SALTY salmonella
36	33	27.3	231	1 HBS2_HELHP	HBS2_HELHP helicobacte
37	33	27.3	253	2 Q6W4C2	Q6W4C2 drosophila
38	33	27.3	253	2 Q6W4C3	Q6W4C3 drosophila
39	33	27.3	253	2 Q6W4B3	Q6W4B3 drosophila
40	33	27.3	258	2 Q6C7G0	Q6C7G0 yarowia 11
41	33	27.3	350	2 Q6PEX1	Q6PEX1 acinetobact
42	33	27.3	418	2 Q02468	Q02468 drosophila
43	33	27.3	467	1 EUTR_SALTY	EUTR_SALTY salmonella
44	33	27.3	467	1 Q8Z4U1	Q8Z4U1 salmonella
45	33	27.3	468	2 Q6LW58	Q6LW58 photobacter

ALIGNMENTS

RESULT 1	ADNP_RAT	STANDARD;	PRT;	823 AA.
ID	ADNP_RAT			
AC	Q9UKT8;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Activity-dependent neuroprotector (Activity-dependent neuroprotective protein).			
GN	Name=Adnp;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RP	SEQUENCE FROM N.A.			
RA	Dong M., Xu K., Du Y.;			
RT	"Complete sequence of a rat protein containing a femtomolar-activity-dependent neuroprotective peptide."			
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Potential transcription factor. May mediate some of the neuroprotective peptide VIP-associated effects involving normal growth and cancer proliferation.			
CC	-1- SUBCELLULAR LOCATION: Nuclear (Potential).			
CC	-1- INDUCTION: By the neuroprotective peptide VIP.			
CC	-1- SIMILARITY: Contains 1 homeobox domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; AF234680; AAF40431.1; -			
DR	RGD; 71030; Adnp.			
DR	InterPro; IPR001356; Homeobox.			
DR	InterPro; IPR009057; Homeobox-like.			
DR	InterPro; IPR007087; ZnF_C2H2.			
DR	Pfam; PF00046; Homeobox; 1.			
DR	Pfam; PF00096; zf-C2H2; 1.			
DR	SMART; SM00389; HOX; 1.			
DR	SMART; SM00355; ZnF_C2H2; 4.			
DR	PROSITE; PS00027; HOMEBOX_1; FALSE_NRG.			
DR	PROSITE; PS00071; HOMEBOX_2; 1.			
DR	PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.			
DR	PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.			
KW	DNA-binding; Homeobox; Metal-binding; Nuclear protein; Repeat; Transcription regulation; Zinc-finger.			
FT	ZN_FING 167 189			
FT	ZN_FING 209 230			
FT	ZN_FING 232 255			
FT	ZN_FING 342 367			
				C2H2-type 1 (atypical).
				C2H2-type 2.
				C2H2-type 3.
				C2H2-type 4 (atypical).

FT ZN FING 382 406 C2H2-type 5 (atypical).
 KW DNA-BIND 474 534 Homeobox.
 SQ SEQUENCE 823 AA; 91335 MW; A4C4BC16052BDDF CRC64;
 Query Match 33.9%; Score 41; DB 1; Length 823;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIPO 48
 Db 74 NAFVSIPO 81

RESULT 2
 ADNP MOUSE
 ID ADNP MOUSE STANDARD; PRT; 828 AA.
 AC 092103;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Activity-dependent neuroprotector (Activity-dependent neuroprotective protein).
 GN Name=Adnp;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SYNTHESIS OF 74-81.
 RC TISSUE=Brain;
 RX MEDLINE=99155106; PubMed=10037502;
 RA Bassan M., Zamostiano R., Davidson A., Pinhasov A., Giladi E., Perl O., Bassan H., Blat C., Gabney G., Glazner G., Brenneman D.E., Gozes I.;
 RA "Complete sequence of a novel protein containing a fentomolar-activity-dependent neuroprotective peptide.";
 RT J. Neurochem. 72:1283-1293(1999).
 RL -1- FUNCTION: Potential transcription factor. May mediate some of the neuroprotective peptide VIP-associated effects involving normal growth and cancer proliferation.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed in the brain, with a higher expression in cerebellum and hippocampus. Weakly expressed in lung, kidney and intestine, and expressed at intermediate level in testis.
 CC -1- INDUCTION: By the neuroprotective peptide VIP.
 CC -1- MISCELLANEOUS: When isolated from the sequence, the neuroprotective peptide provides neuroprotection at subfemtomolar concentrations against toxicity associated with tetrodotoxin (electrical blockade), the beta-amyloid peptide (the Alzheimer's disease neurotoxin), N-methyl-D-aspartate (excitotoxicity), and the human immunodeficiency virus (HIV) envelope protein.
 CC -1- SIMILARITY: Contains 1 homeobox domain.
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 CC EMBL; AF068198; AAD19843.1; -
 CC MGD; MGI:1338758; Adnp.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR009057; Homeobox-like.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00046; Homeobox; 1.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00355; ZNF_C2H2; 4.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
 KW DNA-Binding; Homeobox; Metal-binding; Nuclear protein; Repeat;
 KM Transcription regulation; Zinc-finger.
 FT ZN FING 166 188 C2H2-type 1 (atypical).
 FT ZN FING 208 229 C2H2-type 2.
 FT ZN FING 231 254 C2H2-type 3.
 FT ZN FING 341 366 C2H2-type 4 (atypical).
 FT ZN FING 381 405 C2H2-type 5 (atypical).
 FT DNA BIND 473 533 Homeobox.
 FT SITE 74 81 Neuroprotective peptide.
 FT DOMAIN 599 670 Glu-rich.
 SQ SEQUENCE 828 AA; 92063 MW; 9DFE69C506B8606 CRC64;

Query Match 33.9%; Score 41; DB 1; Length 828;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIPO 48
 Db 74 NAFVSIPO 81

RESULT 3

06ZQ47 PRELIMINARY; PRT; 1089 AA.

AC 06ZQ47;
 DT 05-JUL-2004 (TRENBLREL. 27, Created)
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE MKIA0784 protein (Fragment).
 GN Name=MKIA0784;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX PubMed=14621295;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Suga Y., Nagase T., Ohara O., Koga H.;
 RA "Prediction of the coding sequences of mouse homologues of KIAA gene: III. the complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";
 RT RNA Res. 10:167-180(2003).
 RL -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC EMBL; AK129214; BAC98024.1; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0008270; P:zinc ion binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00046; Homeobox; 1.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00355; ZNF_C2H2; 8.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
 KW DNA-Binding; Homeobox; Nuclear protein.
 FT NON TER 1
 SQ SEQUENCE 1089 AA; 122152 MW; 7FF389C7FAEDF660 CRC64;

Query Match 33.9%; Score 41; DB 2; Length 1089;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIPO 48
 Db 335 NAFVSIPO 342

RESULT 4
ADNP HUMAN STANDARD; PRT; 1102 AA.
ID ADNP_HUMAN 094881; 09UG34;
AC 09H2B0; 094881; 09UG34;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Activity-dependent neuroprotector (Activity-dependent neuroprotective protein).
GN Name-ADNP; Synonyms=KIAA0784;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RX TISSUE=Brain;
RX PubMed=1103255; DOI=10.1074/jbc.M007416200;
RX Zamostiano R., Pinhasov A., Gelber E., Steinart R.A., Serousi E., Giladi E., Baasan M., Wollman Y., Eyre H.J., Mulley J.C., Breneman D.E., Gozes I.;
RA "Cloning and characterization of the human activity-dependent neuroprotective protein.";
RT J. Biol. Chem. 276:708-714(2001).
[2]
SEQUENCE FROM N.A.
RA MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R., Jones M., Scavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D.J., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Cowley G.J., Deadman R., Dhami P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Leharasaito M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McCannachie L.J., McElay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prabhalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
[3]
SEQUENCE OF 30-1102 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99087487; PubMed=9872452;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
RL DNA Res. 5:277-286(1998).
[4]
SEQUENCE OF 98-1102 FROM N.A.
RC TISSUE=Uterus;
RA Mamout R., Heubner D., Mewes H.-W., Gassenhuber J., Wiemann S.;
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Potential transcription factor. May mediate some of the neuroprotective peptide VIP-associated effects involving normal growth and cancer proliferation.

CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- TISSUE SPECIFICITY: Widely expressed. Strong expression in heart, skeletal muscle, kidney and placenta. In brain, expression is stronger in the cerebellum and cortex regions. No expression detected in the colon. Strong increase of expression in colon and breast cancer tissues.
CC -!- SIMILARITY: Contains 1 homeobox domain.
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CC -----
CC EMBL; AF250860; AAG47651.1; -;
CC EMBL; AL034553; CAB53748.2; -;
CC EMBL; AB018327; BAA34504.1; -;
CC EMBL; AL080163; CAB45752.1; -;
CC PIR; T12546; T12546.
CC Genew; HGNC:15765; ADNP.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR009057; Homeoboxdomain_like.
CC DR Pfam; PF00046; Homeobox; 1.
CC DR Pfam; PF00096; zf-C2H2; 2.
CC SMART; SM00389; HOX; 1.
CC SMART; SM00355; ZNF_C2H2; 8.
CC PROSITE; PS00027; HOMEBOX_1; FALSE_NEG.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
CC PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
CC KW DNA-binding; Homeobox; Metal-binding; Nuclear protein; Repeat; Transcription regulation; Zinc-finger.
KW ZN_FING 74
FT ZN_FING 107 129 C2H2-type 1 (atypical).
FT ZN_FING 165 188 C2H2-type 3.
FT ZN_FING 221 244 C2H2-type 4.
FT ZN_FING 447 469 C2H2-type 5 (atypical).
FT ZN_FING 469 510 C2H2-type 6 (atypical).
FT ZN_FING 512 535 C2H2-type 7.
FT ZN_FING 622 647 C2H2-type 8 (atypical).
FT ZN_FING 662 686 C2H2-type 9 (atypical).
FT DNA_BIND 754 814 Homeobox.
SQ SEQUENCE 1102 AA; 123562 MW; 4132E3EF81AF43B CRC64;
Query Match 33.9%; Score 41; DB 1; Length 1102;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 NAPVSIQ 48
DB 354 NAPVSIQ 361
RESULT 5
Q6DHZ8 PRELIMINARY; PRT; 1102 AA.
ID Q6DHZ8
AC 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Activity-dependent neuroprotector.
GN Name-ADNP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RX TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mollahy S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL: BC075794; AAF75794.1; -.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR003439; ABC transporter.
 DR InterPro: IPR001355; Homeobox.
 DR InterPro: IPR009057; Homeodomain-like.
 DR InterPro: IPR007087; Znf_C2H2.
 DR Pfam: PF00046; Homeobox; 1.
 DR Pfam: PF00096; zf-C2H2; 1.
 DR SMART: SM00355; HOK; 1.
 DR SMART: SM00355; Znf_C2H2; 8.
 DR PROSITE: PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
 DR PROSITE: PS50071; HOMEBOX_2; 1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 1.
 DR DNA-binding; Homeobox; Nuclear protein.
 KW SEQUENCE 1102 AA; 123446 MW; 286984E554DC766A CRC64;

Query Match 33.9%; Score 41; DB 2; Length 1102;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIPO 48
 DB 354 NAFVSIPO 361

RESULT 6
 ID 06C9B5 PRELIMINARY; PRT; 445 AA.
 AC 06C9B5;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Similar to DEHA0D16797 Debaryomyces hansenii.
 GN ORFNames=YAL10D12496G;
 OS Yarrowia lipolytica CLIB99.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OC NCBI_TaxID=284591;
 RX [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Bianchini S., Beckerich J.M., Beyne E., Blaykassen C.,
 RA Bostane A., Boyer J., Catolico L., Confalonieri F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantoune F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaitre M., Lesur I., Ma L., Muller H.,
 RA Nicard J.M., Nikolski M., Ozas S., Ozler-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swenne D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Cautron B., Scaupelli C., Gallardin C., Weissbach J.,
 RA Wincker P., Souciet J.L.;
 RA "Genome evolution in yeasts.";
 RT Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CR382130; CAG80935.1; -.
 SO SEQUENCE 445 AA; 50191 MW; DB039F405D2D9BBC CRC64;

Query Match 29.8%; Score 36; DB 2; Length 445;
 Best Local Similarity 75.0%; Pred. No. 72;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAFVSIPO 48
 DB 310 NAFVSIPO 317

RESULT 7
 ID 082YW3 PRELIMINARY; PRT; 470 AA.
 AC 082YW3;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 GN Citrate lyase, alpha subunit.
 DE Citrate lyase, OrderedLocNames=EF3319;
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OC NCBI_TaxID=1351;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=V583 / ATCC 700802;
 RX MEDLINE=22550857; PubMed=1263927; DOI=10.1126/science.1080613;
 RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Sehnadi R.,
 RA Read T.D., Fouts D.E., Eissen J.A., Gill S.R., Heidelberg J.F.,
 RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beaman M.J.,
 RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
 RA Khouli H.M., Uterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
 RA Fraser C.M.;
 RT "Role of mobile DNA in the evolution of vancomycin-resistant
 RT Enterococcus faecalis.";
 RL Science 299:2071-2074(2003).
 DR EMBL: AE016957; AAO82984.1; -.
 DR TIGR: EF3319; -.
 DR GO: GO:0009346; C:citrate lyase complex; IEA.
 DR GO: GO:0008814; F:citrate CoA-transferase activity; IEA.
 DR GO: GO:0006084; P:acetyl-CoA metabolism; IEA.
 DR InterPro: IPR006472; CitF.
 DR Pfam: PF04223; CitF; 1.
 DR PIRSF: PIRSF009451; CitF_lyas_alpha; 1.
 DR TIGRfam: TIGR01584; citF; 1.
 KW Complete proteome.
 SO SEQUENCE 470 AA; 50138 MW; 80B3116774432C93 CRC64;

Query Match 29.8%; Score 36; DB 2; Length 470;
 Best Local Similarity 75.0%; Pred. No. 77;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAPVISIPQ 48
|:|||||
Db 175 NTPISIPQ 182

RESULT 8

Q98338 PRELIMINARY; PRT; 481 AA.
AC O8E338;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2004 (TEMBLrel. 23, Last sequence update)
DE Hypothetical protein gbs1925.
GN OrderedlocusNames=gbs1925;
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaeser P., Ruenliok C., Buchrieser C., Chevalier F., Frangeul L.,
RA Msadek T., Zouine M., Couve E., Lailouli L., Foyart C., Trieu-Cuot P.,
RA Kunet F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL MOL. Microbiol. 45:1489-1513(2002).
DR EMBL; AL766854; CAD47584.1; -.
DR Sagalier; gbs1925; -.
DR InterPro; IPR006270; Strept_his_triad.
DR Pfam; PF04270; Strept_his_triad; 4.
DR TIGRPFAM; TIGR01363; strep_his_triad; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 53326 MW; DFDFO453D8A929BE CRC64;

Query Match 29.8%; Score 36; DB 2; Length 481;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAPVISIPQ 48
|:|||||
Db 281 NAPISIPR 288

RESULT 9

Q98P023 PRELIMINARY; PRT; 510 AA.
AC O8P023;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Putative citrate lyase, alpha subunit.
GN Name=citF; OrderedlocusNames=spyM18_1140;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS823;
RX MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.B., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
DR EMBL; AE010039; AL97760.1; -.
DR GO; GO:0009346; Citrate lyase complex; IEA.

DR GO; GO:0008814; F.citrate CoA-transferase activity; IEA.
DR GO; GO:0005489; F.election transporter activity; IEA.
DR GO; GO:0016829; F.lyase activity; IEA.
DR GO; GO:0006084; P.acetyl-CoA metabolism; IEA.
DR GO; GO:0006118; P.election transport; IEA.

DR InterPro; IPR006472; CitF.
DR InterPro; IPR000049; ETF_beta.
DR Pfam; PF04223; CitF; 1.
DR PIRSF; PIRSF009451; CitF_lyas_alpha; 1.
DR ProDom; PD003528; ETF_beta; 1.
DR TIGRPFAM; TIGR01584; citF; 1.
KW Complete proteome; Lyase.
SQ SEQUENCE 510 AA; 54918 MW; 05F3E30FDBAD4DF CRC64;

Query Match 29.8%; Score 36; DB 2; Length 510;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAPVISIPQ 48
|:|||||
Db 215 NTPISIPQ 222

RESULT 10

Q992K7 PRELIMINARY; PRT; 510 AA.
AC O992K7;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Putative citrate lyase, alpha subunit (EC 4.1.3.6).
GN Name=citF; OrderedlocusNames=SPY1189;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=SP370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
RA Ferrerelli J.J., Mcshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar P.Z., Ren Q., Zhu R., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.B.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006559; AK34053.1; -.
DR GO; GO:0009346; Citrate lyase complex; IEA.
DR GO; GO:0008815; F.citrate (pro-3S)-lyase activity; IEA.
DR GO; GO:0008814; F.citrate CoA-transferase activity; IEA.
DR GO; GO:0016829; F.lyase activity; IEA.
DR GO; GO:0006084; P.acetyl-CoA metabolism; IEA.
DR InterPro; IPR006472; CitF.
DR Pfam; PF04223; CitF; 1.
DR PIRSF; PIRSF009451; CitF_lyas_alpha; 1.
DR TIGRPFAM; TIGR01584; citF; 1.
KW Complete proteome; Lyase.
SQ SEQUENCE 510 AA; 54990 MW; 459833B693E2EFA7 CRC64;

Query Match 29.8%; Score 36; DB 2; Length 510;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAPVISIPQ 48
|:|||||
Db 215 NTPISIPQ 222

RESULT 11

Q8K7F1 PRELIMINARY; PRT; 510 AA.
ID O8K7F1;
AC O8K7F1; Q79X56;
DT 01-OCT-2002 (TEMBLrel. 22, Created)

```

DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
GN Putative citrate lyase, alpha subunit.
GN Name=citF; OrderedLocNames=SPB1034; SpvM3_0834;
OC Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OK NCBI_Taxid=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Bers S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phase-encoded toxins, the high-virulence phenotype, and clone
RT emergence."
RT Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution."
RT Genome Res. 13:1042-1055(2003).
DR EMBL; AE014153; AAM79441.1; -.
DR GO; GO:0009346; Citrate lyase complex; IEA.
DR GO; GO:0008814; Fcitrates CoA-transferase activity; IEA.
DR GO; GO:0005489; Fcitrates transporter activity; IEA.
DR GO; GO:0016829; Fcitrates activity; IEA.
DR GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006472; CitF.
DR InterPro; IPR000049; ETF_beta.
DR Pfam; PF04223; CitF; 1.
DR PIRSF; PIRSF009451; CitF_lyase_alpha; 1.
DR PRODOM; PD003528; ETF_beta; 1.
DR TIGRFAMs; TIGR01584; CitF; 1.
KM Lyase; Complete proteome.
SQ SEQUENCE 510 AA; 54890 MW; F84036B9F2B0D9A8 CRC64;

Query Match 29.8%; Score 36; DB 2; Length 510;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAFVSIPQ 48
DB 215 NTPISIPQ 222

RESULT 12
OBDUCT1 PRELIMINARY; PRT; 511 AA.
AC OBDUCT1;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 25, Last annotation update)
DE Putative citrate lyase, alpha subunit (BC 4.1.3.6).
GN Name=citA; OrderedLocNames=SMU.1021;
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DA159 / ATCC 700610 / Serotype c;

```

```

RX MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
RA Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans DA159, a cariogenic dental
RT pathogen."
RT Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
DR EMBL; AE014941; AAN58721.1; -.
DR GO; GO:0009346; Citrate lyase complex; IEA.
DR GO; GO:0008814; Fcitrates (pro-3S)-lyase activity; IEA.
DR GO; GO:0008814; Fcitrates CoA-transferase activity; IEA.
DR GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
DR InterPro; IPR006472; CitF.
DR Pfam; PF04223; CitF; 1.
DR PIRSF; PIRSF009451; CitF_lyase_alpha; 1.
DR TIGRFAMs; TIGR01584; CitF; 1.
KM Complete proteome.
SQ SEQUENCE 511 AA; 55455 MW; FP966EB258334174 CRC64;

Query Match 29.8%; Score 36; DB 2; Length 511;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAFVSIPQ 48
DB 215 NTPISIPQ 222

RESULT 13
OBDUCT1 PRELIMINARY; PRT; 631 AA.
AC OBDUCT1;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=PA1941;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OK NCBI_Taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lapidis K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RT Nature 406:959-964(2000).
DR EMBL; AE004620; AAG05323.1; -.
DR PIR; B83404; B83404.
DR InterPro; IPR000345; Cytochrome_B5.
DR InterPro; IPR009056; Cytochrome_C.
DR PROSITE; PS00190; CYTOCHROME_C_UNKNOWN_2.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 631 AA; 70904 MW; E72A4692AEB75F1 CRC64;

Query Match 29.8%; Score 36; DB 2; Length 631;
Best Local Similarity 87.5%; Pred. No. 11e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAFVSIPQ 48
DB 263 NAFVSIPQ 270

RESULT 14

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O6KAS0
ID O6KAS0 PRELIMINARY; PRT; 1396 AA.
AC O6KAS0;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE MFL00137 protein (Fragment).
GN Name=MFL00137;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Okazaki N., Kitumura R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Suga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.,
RT "Prediction of the Coding Sequences of Mouse Homologues of F1J Genes:
RT The Complete Nucleotide Sequences of 110 Mouse Full-Homologous cDNAs
RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly
RT Sampled from Size-Fractionated Libraries."
RL DNA Res. 11:167-180(2004).
CC -1- SIMILARITY: Contains 9 WD repeats.
DR EMBL; AK131137; BAF21387.1; -.
DR InterPro; IPR002114; HPr_Serp_S.
DR InterPro; IPR011680; WD40.
DR Pfam; PF00400; WD40_1like.
DR PRINTS; PR00320; GPROTEINRPT.
DR PRODOM; PD000018; WD40; 1.
DR SMART; SM00320; WD40; 1.
DR PROSITE; PS00569; PTS_HPR_SER; UNKNOWN 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 2.
DR PROSITE; PS50294; WD_REPEATS_2; 2.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KM Repeat; WD repeat.
FT NON_TER 1
SQ SEQUENCE 1396 AA; 155525 MW; 1B6851D794FB06A0 CRC64;

Query Match 29.8%; Score 36; DB 2; Length 1396;
Best Local Similarity 75.0%; Pred. NO. 2.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIQ 48
Db 1314 NAFVSLPE 1321

RESULT 15
GEMS_MOUSE STANDARD; PRT; 1502 AA.
AC O8BX17;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Gem-associated protein 5 (Gemins).
GN Name=Gemin5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA MEDLINE=22354663; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikiido I., Osato N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chotina C., Cortant L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

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RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A.,
RA Maglott D.R., Maltre L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan M.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai K., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
RA Sultana R., Takemura Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wymahaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
CC -1- FUNCTION: The SMN complex plays an essential role in spliceosomal
CC snRNP assembly in the cytoplasm and is required for pre-mRNA
CC splicing in the nucleus.
CC -1- SUBUNIT: Part of the core SMN complex that contains SMN1, SMN2,
CC GEMIN2, GEMIN4, GEMIN5, GEMIN6 and GEMIN7. Interacts
CC directly with SMN1, SNRNP, SNRPD1, SNRPD2, SNRPD3 and SNRPE (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear, found both in the nucleoplasm and
CC in nuclear bodies called gems (gemini of Cajal bodies) that are
CC often in proximity to Cajal (coiled) bodies. Also found in the
CC cytoplasm (By similarity).
CC -1- SIMILARITY: Contains 13 WD repeats.
CC
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AK049216; BAC3614.1; -.
DR MGI; MGI:2449311; Gemin5.
DR InterPro; IPR011048; Cyt_cdl_haem_C.
DR InterPro; IPR008941; TPR-like.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 1.
DR PRINTS; PR00320; GPROTEINRPT.
DR PRODOM; PD000018; WD40; 1.
DR SMART; SM00320; WD40; 13.
DR PROSITE; PS00678; WD_REPEATS_1; 3.
DR PROSITE; PS50294; WD_REPEATS_2; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KM Coiled coil; mRNA processing; mRNA splicing; Nuclear protein; Repeat;
KW Spliceosome; WD repeat.
FT REPEAT 62 104 WD 1.
FT REPEAT 107 148 WD 2.
FT REPEAT 150 189 WD 3.
FT REPEAT 193 264 WD 4.
FT REPEAT 280 321 WD 5.
FT REPEAT 333 374 WD 6.
FT REPEAT 377 417 WD 7.
FT REPEAT 424 464 WD 8.
FT REPEAT 468 509 WD 9.
FT REPEAT 533 573 WD 10.
FT REPEAT 576 622 WD 11.
FT REPEAT 637 677 WD 12.
FT REPEAT 680 720 WD 13.
FT DOMAIN 738 746 Poly-Iys.
FT DOMAIN 1355 1382 Coiled coil (Potential).
SQ SEQUENCE 1502 AA; 165562 MW; 46F98CCE70E2971 CRC64;

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Query Match 29.8%; Score 36; DB 1; Length 1502;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAPVSIPO 48
1420 NAPVSLPE 1427

Search completed: February 23, 2005, 19:34:18
Job time : 116.35 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 23, 2005, 19:22:32 ; Search time 24.3616 Seconds
(without alignments)
347,559 Million cell updates/sec

Title: US-09-267-511-4

Perfect score: 121

Sequence: 1 XXX 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	33.9	1005	2	T12546
2	36	29.8	631	2	B83404
3	35	28.9	399	2	D95412
4	34	28.1	136	2	G69440
5	34	28.1	1272	2	T30248
6	33	27.3	198	2	A10632
7	33	27.3	467	2	AH0813
8	33	27.3	479	2	H86465
9	33	27.3	601	2	S47896
10	33	27.3	1119	2	T50995
11	33	27.3	1213	2	S16356
12	33	27.3	2251	2	T24490
13	32	26.4	97	2	T25754
14	32	26.4	249	2	AE1928
15	32	26.4	301	2	AE0243
16	32	26.4	400	2	T47111
17	32	26.4	657	2	F97604
18	32	26.4	668	2	AH2826
19	32	26.4	1017	2	B70985
20	32	26.4	2774	2	A43359
21	32	26.6	159	2	C81662
22	31	25.6	263	2	C83959
23	31	25.6	341	2	T35027
24	31	25.6	350	2	AE0637
25	31	25.6	358	2	B81194
26	31	25.6	358	2	A81831
27	31	25.6	392	2	T51772
28	31	25.6	393	2	C89601
29	31	25.6	393	2	S72804

30	31	25.6	394	2	B48376	acetyl-CoA C-acetyl
31	31	25.6	395	2	AG2606	conserved hypochet
32	31	25.6	395	2	F97388	probable lipase (A
33	31	25.6	424	2	T14728	probable betaine-a
34	31	25.6	459	2	D34791	interleukin-7 rece
35	31	25.6	504	2	T16526	hypothetical prote
36	31	25.6	518	2	F89888	conserved hypochet
37	31	25.6	558	1	B28392	penicillin amidase
38	31	25.6	558	2	S27199	cephalosporin acyl
39	31	25.6	679	2	T52163	hypothetical prote
40	31	25.6	787	2	T41974	replication origin
41	31	25.6	881	2	RG87G4	regulatory protein
42	31	25.6	936	1	S57637	hexon protein - hu
43	31	25.6	952	1	HXAD5	hexon protein - hu
44	31	25.6	967	1	HXAD2	hexon protein - hu
45	31	25.6	2512	2	E70751	probable ntp prote

ALIGNMENTS

RESULT 1
T12546
hypothetical protein DKFZp586K2120.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C/Accession: T12546
R/Mambult, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A/Reference number: Z17524
A/Accession: T12546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1005 <MAN>
A/Cross-references: UNIPROT:Q9H220; EMBL:AL080163
A/Experimental source: adult uterus; clone DKFZp586K2120
C/Genetics:
A/Note: DKFZp586K2120.1

Query Match 33.9%; Score 41; DB 2; Length 1005;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAPVSIPQ 48
DB 257 NAPVSIPQ 264

RESULT 2

B83404
hypothetical protein PA1941 [imported] - Pseudomonas aeruginosa (strain PAO1)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C/Accession: B83404

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path

A/Reference number: AB2950; MUID:20437337; PMID:10984043

A/Accession: B83404

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-631 <STO>

A/Cross-references: UNIPROT:Q912G3; GB:AE004620; GB:AE004091; NID:g9947929; PIDN:AA0053.

A/Experimental source: strain PAO1

C/Genetics:

A/Genes: PA1941

Query Match 29.8%; Score 36; DB 2; Length 631;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAPVSIPQ 48
 |||||
 Db 263 NAPVSYPQ 270

RESULT 3

D95412
 hypothetical protein SMA2233 [imported] - Sinorhizobium meliloti (strain 1021) magaplast
 C/Species: Sinorhizobium meliloti
 C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C/Accession: D95412

R;Barrett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Aboja, A.P.; Barloy-Hubler, F.; Bows
 ; Katman, S.; Keating, D.H.; Palm, C.; Beck, M.C.; Surzycki, R.; Wells, D.H.; Yen, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A/Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
 A/Reference number: A95262; MUID:21396509; PMID:11481432
 A/Accession: D95412

A/Status: preliminary
 A/Molecule type: DNA

A/Residues: 1-299 <KUR>

A/Cross-references: UNIPROT:Q92XP0; GB:AE006469; PIDN:AK65862.1; PID:gl4524369; GSPDB:C

A/Experimental source: strain 1021, megaplastid pSymbA

R;Galbert, F.; Finn, T.M.; Long, S.R.; Puhler, A.; Aboja, P.; Ampe, F.; Barloy-Hubler,
 pela, D.; Chait, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaul, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weiss, D.H.; Wong, K.; Yen, K.

A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A/Reference number: A96039; MUID:21368234; PMID:11474104

A/Contents: annotation
 C/Genetics:
 A/Gene: SMA2233
 A/Genome: plasmid

Query Match 28.1%; Score 35; DB 2; Length 299;
 Best Local Similarity 100.0%; Pred. No. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 APVSIPQ 48
 |||||
 Db 6 APVSIPQ 12

RESULT 4

G69440
 conserved hypothetical protein AF1528 - Archaeoglobus fulgidus

C/Species: Archaeoglobus fulgidus
 C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C/Accession: G69440

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kinkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A/Authors: Utecher, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Weese, C.R.; Venter, J.C.

A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A/Reference number: A69250; MUID:96049343; PMID:9389475

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA
 A/Residues: 1-136 <KLE>
 A/Cross-references: UNIPROT:O28744; GB:AE000997; GB:AE000782; NID:g2689320; PIDN:AB8972

Query Match 28.1%; Score 34; DB 2; Length 136;
 Best Local Similarity 75.0%; Pred. No. 9.3;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAPVSIPQ 48
 |||||
 Db 29 NAPVSIPQ 36

RESULT 5

T30248
 fragile X mental retardation protein 2 - mouse

N/Alternate names: fmr2 protein

C/Species: Mus musculus (house mouse)

C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T30248

R;Chakrabarti, L.; Bristulf, J.; Foss, G.S.; Davies, K.E.

Hum. Mol. Genet. 7, 441-448, 1998

A/Title: Expression of the murine homologue of FMR2 in mouse brain and during developmen

A/Reference number: Z20786; MUID:9613924; PMID:9467002

A/Accession: T30248

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1272 <CHA>

A/Cross-references: UNIPROT:O55112; EMBL:AJ001549; NID:g2832399; PIDN:CAA04821.1; PID:g2

A/Experimental source: Brain

C/Genetics:
 A/Gene: fmr2
 A/Note: fmr2 expression in an embryo at 11 days is evident to the roof of the hind brain

Query Match 28.1%; Score 34; DB 2; Length 1272;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAPVSIPQ 48
 |||||
 Db 1191 NCPVITPQ 1198

RESULT 6

A10632
 trp repressor binding protein [imported] - Salmonella enterica subsp. enterica serovar Typh

C/Species: Salmonella enterica subsp. enterica serovar Typh

A/Note: this species has also been called Salmonella typh

C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C/Accession: A10632

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A/Reference number: AB0502; MUID:21534947; PMID:11677608

A/Accession: A10632

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-198 <PAR>

A/Cross-references: GB:AL513382; PIDN:CAD08244.1; PID:gl6502291; GSPDB:GN00176

C/Genetics:
 A/Gene: STY1155
 C/Superfamily: trp repressor-binding protein; flavodoxin homology
 C/Keywords: Flavoprotein

Query Match 27.3%; Score 33; DB 2; Length 198;
 Best Local Similarity 75.0%; Pred. No. 23;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAPVSIPQ 48
 |||||
 Db 57 NAPVSIPQ 64

RESULT 7

AH0813
 probable ethanolamine utilization protein EutA eutA [imported] - Salmonella enterica sub

C/Species: Salmonella enterica subsp. enterica serovar Typh

A/Note: this species has also been called Salmonella typh

C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C/Accession: AH0813

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A/Reference number: AB0502; MUID:21534947; PMID:11677608

A/Accession: A10632

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-198 <PAR>

A/Cross-references: GB:AL513382; PIDN:CAD08244.1; PID:gl6502291; GSPDB:GN00176

C/Genetics:
 A/Gene: STY1155
 C/Superfamily: trp repressor-binding protein; flavodoxin homology
 C/Keywords: Flavoprotein

Query Match 27.3%; Score 33; DB 2; Length 198;
 Best Local Similarity 75.0%; Pred. No. 23;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAPVSIPQ 48
 |||||
 Db 57 NAPVSIPQ 64

Nature 413, 848-852, 2001
A:Author: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A:Reference number: AB0502; NCID:21534947; PMID:11677608
A:Accession: AH0813
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-467 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07690.1; PID:gl6503676; GSPDB:GN00176
C:Genetics:
A:Gene: *eutA*
C:Superfamily: *Escherichia coli* hypothetical protein b2451

Query Match 27.3%; Score 33; DB 2; Length 467;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAFVSIPO 48
DB 338 NAFVSIPO 345

RESULT 8
H66465
F12G12.1 protein - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #ext_change 09-Jul-2004
C:Accession: H66465
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzler, L.
Nature 408, 816-820, 2000
A:Author: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sekano, H.
A:Author: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: AB6141; NCID:21016719; PMID:11130712
A:Accession: H66465
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <STO>
A:Cross-references: UNIPROT:Q9FX25; GB:AE005172; NCID:g10086460; PIDN:AAG12520.1; GSPDB:G
C:Genetics:
A:Map position: 1

Query Match 27.3%; Score 33; DB 2; Length 479;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIPO 48
DB 303 NSPISVPE 310

RESULT 9
S47896
probable molybdopterin biosynthesis protein cinnamon - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 12-Jul-2004
C:Accession: S47896
R:Kamdar, K.P.; Shelton, M.E.; Finnerty, V.
Genetics 137, 791-801, 1994
A:Title: The *Drosophila* molybdenum cofactor gene cinnamon is homologous to three *Escheri*
A:Reference number: S47896; NCID:94374679; PMID:8088525
A:Accession: S47896
A:Molecule type: mRNA
A:Residues: 1-601 <KAM>
A:Cross-references: EMBL:L19876; NCID:g979288; PIDN:AAA68677.1; PID:g505312
A:Experimental source: developmental stage embryo
C:Genetics:
A:Gene: *flyBase:cinn*

A:Cross-references: *FlyBase:FBgn0000316*
C:Function:
A:Pathway: molybdopterin biosynthesis
C:Superfamily: bifunctional molybdenum cofactor biosynthesis protein, Gephyrin type
C:Keywords: molybdopterin biosynthesis; multifunctional enzyme; transmembrane protein

Query Match 27.3%; Score 33; DB 2; Length 601;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIPO 47
DB 226 NAFVSIPO 232

RESULT 10
T50995
related to cytoskeleton assembly control protein SLAI [imported] - *Neurospora crassa*
N:Alternate names: protein B7F18.140
C:Species: *Neurospora crassa*
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #ext_change 09-Jul-2004
C:Accession: T50995
R:Schulte, U.; Aign, V.; Hohnsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, July 2000
A:Reference number: Z25286
A:Accession: T50995
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1119 <SCH>
A:Cross-references: UNIPROT:Q9P3N5; EMBL:AL389891; GSPDB:GN00116; NCSP:B7F18.140
A:Experimental source: BAC clone B7F18; strain OR74A
C:Genetics:
A:Gene: NCSP:B7F18.140
A:Map position: 6/3; 123/2; 495/1
A:Introns: 66/3; 123/2; 495/1

Query Match 27.3%; Score 33; DB 2; Length 1119;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 42 APVSIPO 48
DB 157 APVSIPO 163

RESULT 11
S16356
ovo protein - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 09-Jul-2004
C:Accession: S16356
R:Mevel-Ninio, M.; Terracol, R.; Kafatos, F.C.
EMBO J. 10, 2259-2266, 1991
A:Title: The *ovo* gene of *Drosophila* encodes a zinc finger protein required for female ge
A:Reference number: S16356; NCID:91293102; PMID:1712294
A:Accession: S16356
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1213 <MEV>
A:Cross-references: UNIPROT:O8T8L9; EMBL:X59772
C:Genetics:
A:Gene: *FlyBase:ovo*
A:Cross-references: *FlyBase:FBgn0003028*
A:Introns: 931/3; 1152/3

Query Match 27.3%; Score 33; DB 2; Length 1213;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIPO 48
DB 46 NSPISIPK 53

RESULT 12

T24490

hypothetical protein T05A10.1 - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T24490

R/Suleton, J.

submitted to the EMBL Data Library, November 1995

A/Reference number: Z19898

A/Accession: T24490

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-2251 <WIL>

A/Cross-references: UNIPROT:Q22190; EMBL:Z68108; PIDN:CAA92133.1; GSPDB:GN00028; CESP:TC

A/Experimental source: clone T05A10

C/Genetics:

A/Map position: X

A/Introns: 188/3; 240/3; 420/1; 570/3; 596/1; 732/3; 778/3; 851/3; 1359/2; 1394/2; 1434/

Query Match 27.3%; Score 33; DB 2; Length 2251;

Best Local Similarity 85.7%; Pred. No. 3.6e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIPO 47

Db 1311 NAFVSIPO 1317

RESULT 13

T25754

hypothetical protein F45E4.5 - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T25754

R/Wilson, R.

submitted to the EMBL Data Library, September 1996

A/Description: The sequence of C. elegans cosmid F45E4.

A/Reference number: Z20082

A/Accession: T25754

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-97 <WIL>

A/Cross-references: UNIPROT:Q94228; EMBL:U70852; PIDN:AB09136.1; GSPDB:GN00022; CESP:F4

A/Experimental source: strain Bristol N2; clone F45E4

C/Genetics:

A/Map position: 4

A/Introns: 34/2; 74/1

Query Match 26.4%; Score 32; DB 2; Length 97;

Best Local Similarity 75.0%; Pred. No. 16;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 41 NAFVSIPO 48

Db 18 NAFVSIPO 25

RESULT 14

AE1928

hypothetical protein al10976 [imported] - *Nostoc* sp. (strain PCC 7120)C/Species: *Nostoc* sp. PCC 7120A/Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C/Accession: AE1928

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasaemoto, S.; Watanabe, A.; Iriyuchi,

Nakazaki, N.; Shimoto, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*

A/Reference number: AB1807; MUID:21595285; PMID:11759840

A/Accession: AE1928

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-249 <KUR>

A/Cross-references: UNIPROT:Q8Y175; GB:BA000019; PIDN:BA072933.1; PID:G17130322; GSPDB:G

A/Experimental source: strain PCC 7120

C/Genetics:

A/Map position: X

A/Introns: 188/3; 240/3; 420/1; 570/3; 596/1; 732/3; 778/3; 851/3; 1359/2; 1394/2; 1434/

Query Match 26.4%; Score 32; DB 2; Length 249;

Best Local Similarity 71.4%; Pred. No. 48;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 41 NAFVSIPO 47

Db 20 NAFVSIPO 26

RESULT 15

AE0243

hypothetical protein YPO1996 [imported] - *Yersinia pestis* (strain CO92)C/Species: *Yersinia pestis*

C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C/Accession: AE0243

R/Parhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

H. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,

Nature 413, 523-527, 2001

A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AE0243

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-301 <KUR>

A/Cross-references: UNIPROT:Q8ZF00; GB:AL590842; PIDN:CAC90809.1; PID:G15980010; GSPDB:G

C/Genetics:

A/Map position: X

A/Introns: 188/3; 240/3; 420/1; 570/3; 596/1; 732/3; 778/3; 851/3; 1359/2; 1394/2; 1434/

Query Match 26.4%; Score 32; DB 2; Length 301;

Best Local Similarity 85.7%; Pred. No. 59;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 NAFVSIPO 47

Db 127 NAFVSIPO 133

Search completed: February 23, 2005, 19:35:04
Job time : 25.3616 secs

CC polynucleotide in biological samples, while the antibodies are useful
 CC therapeutically and to isolate ADNF III polypeptides

XX Sequence 9 AA;

Query Match 33.3%; Score 40; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49

DB 1 SALLRSIPA 9

RESULT 2

ID AAY71142 standard; peptide; 9 AA.

AC AAY71142;

DT 08-SEP-2000 (first entry)

DE Human Activity Dependent Neurotrophic Factor (ADNF)-9 active peptide.

XX Activity Dependent Neurotrophic Factor III; ADNF; human; ADNF; ADNF-9;

KM Activity Dependent Neuroprotective Protein; chromosome 20q13.2; ADNF; autosomal dominant nocturnal frontal-lobe epilepsy; neuronal cell death;

KM neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;

KM Alzheimer's disease; beta-amyloid peptide; Huntington's disease;

KM epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;

KM amyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;

KM mitochondrial abnormality; Wernicke's encephalopathy; homocystinuria;

KM hyperproliferation; sulphite oxidase disease; Tourette's syndrome; nocturnal;

KM Down's syndrome; drug addiction; developmental retardation; epileptic;

KM learning impairment; anticonvulsant; neuroprotective; anti-HIV.

XX Homo sapiens.

XX WO200027875-A2.

XX 18-MAY-2000.

XX 04-NOV-1999; 99WO-US026213.

XX 06-NOV-1998; 98US-00187330.

XX (USAS) GOVERNMENT US REPRESENT AS.

XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

XX Gozes I, Brennehan DE, Bassan M, Zamostiano R;

XX WPI; 2000-376491/32.

XX New nucleic acid encoding an activity dependent neurotrophic factor III

XX (ADNF III) useful in the treatment of neurological deficiencies and for

XX preventing neuronal cell death.

XX Example; Page 5; 136pp; English.

XX The present sequence is the human Activity Dependent Neurotrophic Factor

XX (ADNF)-9 active peptide sequence. The ADNF III-8 or NAP peptide was

XX synthesised based on the structural homology to ADNF-9 peptide and hsp60.

XX It is also used for immunological detection of cloned ADNF III. ADNF III

XX is also called an Activity Dependent Neuroprotective Protein (ADNP). The

XX human gene was mapped to chromosome 20q13.2 and is linked to autosomal

XX dominant nocturnal frontal-lobe epilepsy (ADNFLE) gene. It is expressed

XX in the astrocytes, brain and also in foetal lung and endocrine tissues.

XX This sequence has homology to ADNF I and hsp60, heat shock protein and

XX p11, a DNA repair protein. The ADNF III polypeptides are useful for the

XX treatment of neurological deficiencies and for prevention of neuronal

XX cell death associated with gp120, the envelope protein from HIV; N-methyl

XX -D-Aspartic acid (excito-toxicity); tetrodotoxin (blockage of electrical

XX activity); and beta-amyloid peptide, a substance related to neuronal

CC degeneration in Alzheimer's disease. It is useful for the treatment of

CC Huntington's disease, AIDS dementia complex, epileptic, neuropathic pain

CC syndromes, Parkinson's disease, amyotrophic lateral sclerosis (ALS),

CC mitochondrial abnormalities, Leber's disease, Wernicke's encephalopathy,

CC Alzheimer's disease, homocystinuria, hyperproliferation, sulphite oxidase

CC disease, Tourette's syndrome, oxidative stress induced neuronal death,

CC Down's syndrome, developmental retardation and learning impairments, drug

CC addiction, tolerance and dependency

XX Sequence 9 AA;

Query Match 33.3%; Score 40; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49

DB 1 SALLRSIPA 9

RESULT 3

ID AAB23471 standard; peptide; 9 AA.

AC AAB23471;

DT 22-JUN-2001 (first entry)

DE Activity dependent neurotrophic factor I peptide #3.

XX Activity dependent neurotrophic factor; ADNF; FAS;

KM fetal alcohol syndrome; gene therapy; neurological deficiency;

KM neuronal cell death.

XX Unidentified.

XX WO200053217-A2.

XX 14-SEP-2000.

XX 10-MAR-2000; 2000WO-US006364.

XX 12-MAR-1999; 99US-00267511.

XX (UYRA-) UNIV RAMOT.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Brennehan DE, Spong CY, Gozes I, Bassan M, Zamostiano R;

XX WPI; 2000-601940/57.

XX Treating condition associated with fetal alcohol syndrome in a subject

XX exposed to alcohol in utero or reducing neuronal death, involves

XX administering activity dependent neurotrophic factors I and/or III.

XX Disclosure; Page 51; 65pp; English.

XX The present invention relates to the treatment of a condition associated

XX with foetal alcohol syndrome (FAS), involving administering an activity

XX dependent neurotrophic factor (ADNF). ADNFs of the present invention may

XX also be used to treat neurological deficiencies and prevent neuronal cell

XX death. The present sequence is an ADNF peptide

XX Sequence 9 AA;

Query Match 33.3%; Score 40; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49

DB 1 SALLRSIPA 9

RESULT 4
AAB23469
ID AAB23469 standard; peptide; 9 AA.
XX
AC AAB23469;
XX
DT 22-JAN-2001 (first entry)
XX
DE Activity dependent neurotrophic factor I peptide #1.
XX
KW Activity dependent neurotrophic factor; ADNF; FAS;
KW foetal alcohol syndrome; gene therapy; neurological deficiency;
KW neuronal cell death.
XX
OS Unidentified.
XX
PN WO200053217-A2.
XX
PD 14-SEP-2000.
XX
PF 10-MAR-2000; 2000WO-US006364.
XX
PR 12-MAR-1999; 99US-00267511.
XX
XX (UYRA-) UNIV RAMOT.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Breneman DE, Spong CY, Gozes I, Basran M, Zamostiano R;
XX
DR WPI; 2000-601940/57.
XX
PT Treating condition associated with fetal alcohol syndrome in a subject
PT exposed to alcohol in utero or reducing neuronal death, involves
PT administering activity dependent neurotrophic factors I and/or III.
XX
PS Claim 5; Page 51; 65pp; English.
XX
CC The present invention relates to the treatment of a condition associated
CC with foetal alcohol syndrome (FAS), involving administering an activity
CC dependent neurotrophic factor (ADNF), ADNFs of the present invention may
CC also be used to treat neurological deficiencies and prevent neuronal cell
CC death. The present sequence is an ADNF peptide
XX
SQ Sequence 9 AA;
Query Match 33.3%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 41 SALLRSIPA 49
DB 1 SALLRSIPA 9
RESULT 5
AAB72315
ID AAB72315 standard; peptide; 9 AA.
XX
AC AAB72315;
XX
DT 16-MAY-2001 (first entry)
XX
DE Activity dependent neurotrophic factor I (ADNF I) peptide SEQ ID 1.
XX
KW Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;
KW neuronal cell death; Alzheimer's disease; oxidative stress; VIP;
KW vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.
XX
OS Synthetic.
XX
PN WO200112654-A2.
XX

PD 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US022861.
XX
PR 18-AUG-1999; 99US-0149956P.
XX
XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Breneman DE, Gozes I, Spong CY, Pinhasov A, Giladi E;
XX
DR WPI; 2001-202855/20.
XX
XX Novel Activity Dependent Neurotrophic Factor I useful for treating
PT oxidative stress, reducing neuronal cell death and treating a condition
PT associated with fetal alcohol syndrome.
XX
XX Claim 2; Page 56; 88pp; English.
XX
XX This invention relates to an activity dependent neurotrophic factor I
CC (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72326 represent
CC ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent
CC ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical
CC composition containing either ADNF I or ADNF III are useful for reducing
CC neuronal cell death, e.g. death of spinal cord neurons, hippocampal
CC neurons, cerebral cortical neurons and cholinergic neurons, in a patient
CC infected with a virus, e.g. human immunodeficiency virus (HIV). The
CC neuronal cell death is associated with excitotoxicity induced by N-
CC methyl-D-aspartate (NMDA) stimulation, which is induced by beta-amyloid
CC peptide in an Alzheimer's disease patient, or induced by cholinergic
CC blockade. ADNF I, ADNF III and the pharmaceutical composition are also
CC useful for treating oxidative stress in a patient, for reducing a
CC condition, such as decreased body weight, decreased brain weight,
CC decreased level of vasoactive body weight, decreased brain weight,
CC death, associated with foetal alcohol syndrome
XX
SQ Sequence 9 AA;
Query Match 33.3%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 41 SALLRSIPA 49
DB 1 SALLRSIPA 9
RESULT 6
AAB07215
ID AAB07215 standard; peptide; 9 AA.
XX
AC AAB07215;
XX
DT 26-MAR-2002 (first entry)
XX
DE ADNF I polypeptide active core site peptide sequence.
XX
KW ADNF, Activity Dependent Neurotrophic Factor; neurotrophic; neuroprotective;
KW cerebroprotective; antidiabetic; neuroleptic; anticonvulsant; anti-HIV;
KW antiparkinsonian; tranquilizer; antialcoholic; vlnenary; antibacterial;
KW antiinflammatory; antidote; ophthalmological; muscular; vasodilator;
KW NMDA receptor.
XX
OS Synthetic.
XX
PN WO200192333-A2.
XX
PD 06-DEC-2001.
XX
PR 31-MAY-2001; 2001WO-US017758.
XX
XX 31-MAY-2000; 2000US-0208944P.
PR 08-FEB-2001; 2001US-0267805P.
XX

PA	(VYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.
PT	
XX	Spong CY, Brennenman D, Gozee I;
XX	WPI; 2002-114330/15.
DR	
XX	
PT	Use of an activity dependent neurotrophic factor for improving learning
XX	and/or memory in a subject by pre- or post-natal administration.
PS	Claim 1, Page 51; 80pp; English.
XX	
XX	The invention provides a method of improving learning and/or memory in a
CC	subject that involves administering pre- or postnatally an Activity
CC	Dependent Neurotrophic Factor (ADNF) to the subject. The ADNF polypeptide
CC	is an ADNF I and/or an ADNF III polypeptide comprising the core active
CC	site sequences ABR07215 or ABR07216. The method is useful for improving
CC	learning and/or memory in a subject; for treating a normal or old subject
CC	afflicted with neuropathology, Alzheimer's disease, Down's syndrome,
CC	normal mental capacity, mental retardation, for the treatment of central
CC	motor systems including degenerative conditions affecting the basal
CC	ganglia (such as Huntington's disease, Wilson's disease, striatonigral
CC	degeneration, corticobasal ganglionic degeneration), Tourette's syndrome,
CC	Parkinson's disease, progressive supranuclear palsy, progressive bulbar
CC	palsy, familial spastic paraplegia, spinomuscular atrophy, dentatorubral
CC	atrophy, olivopontocerebellar atrophy, paraneoplastic cerebellar
CC	degeneration, dopamine toxicity, diseases affecting sensory neurons such
CC	as Friedreich's ataxia, diabetes, peripheral neuropathy, retinal neuronal
CC	degeneration, diseases of limbic and cortical systems such as cerebral
CC	amyloidosis, Pick's atrophy, Rets syndrome, neurodegenerative
CC	pathologies involving multiple neuronal systems and/or brainstem
CC	including AIDS-related dementia, Leigh's disease, diffuse Lewy body
CC	disease, epilepsy, multiple system atrophy, Guillain-Barre syndrome,
CC	lysosomal storage disorders such as lipofuscinosis, late-degenerative
CC	stages of Down's syndrome, Alzheimer's disease, vertigo as a result of CNS
CC	degeneration; pathologies associated with developmental retardation and
CC	learning impairments; oxidative stress induced neuronal death;
CC	pathologies arising with aging and chronic alcohol or drug abuse
CC	including for e.g. with alcoholism the degeneration of neurons in locus
CC	coeruleus, cerebellum, cholinergic basal forebrain; with aging
CC	degeneration of cerebellar neurons and cortical neurons leading to
CC	cognitive and motor impairments; with chronic amphetamine abuse
CC	degeneration of basal ganglia neurons leading to motor impairments;
CC	pathological changes resulting from focal trauma such as stroke, focal
CC	ischemia, vascular insufficiency, hypoxic-ischemia encephalopathy,
CC	hyperglycemia, hypoglycemia, closed head trauma or direct trauma. The
CC	present sequence represents the active core site sequence of the ADNF I
XX	polypeptide
SO	
XX	Sequence 9 AA;
Query Match	33.3%; Score 40; DB 5; Length 9;
Best Local Similarity	100.0%; Pred. No. 1.8e+06;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY	41 SALINSTPA 49
DB	1 SALINSTPA 9
RESULT 7	
ID	ABR39741 standard; peptide; 9 AA.
XX	ABR39741;
AC	
XX	
DT	23-JUN-2003 (first entry)
XX	
DE	ADNF I active core peptide fragment SAL.
XX	
ADNF I	Activity Dependent Neurotrophic Factor I; neuroprotective;
KW	anti-HIV; neuroleptic; antiparkinsonian; nootropic; ADNF-9; SAL.

```

XX XX Unidentified.
XX XX MO2003022226-A2.
XX XX
XX XX 20-MAR-2003.
XX XX
XX XX 12-SEP-2002; 2002MO-US029146.
XX XX
XX XX 12-SEP-2001; 2001US-0322760P.
XX XX
XX XX 10-APR-2002; 2002US-0371961P.
XX XX
XX XX (UTRA-) UNIV RAMOT AT TEL AVIV LTD.
XX XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX XX
XX XX Brenneeman DE, Castellon R, Spong CY, Hauser JM, Gozes I;
XX XX
XX XX WPI; 2003-354501/33.
XX XX
XX XX New Activity Dependent Neurotrophic Factor I complex polypeptide, useful
XX XX for reducing neuronal cell death, treating oxidative stress in a patient,
XX XX or improving learning and/or memory in a subject with e.g. Alzheimer's
XX XX disease.
XX XX
XX XX Disclosure; Page 2; 111pp; English.
XX XX
XX XX The invention relates to Activity Dependent Neurotrophic Factor I (ADNF
XX XX I) complex polypeptide selected from sequences ABR39744-754. The ADNF I
XX XX complex polypeptide is useful for reducing neuronal cell death in
XX XX conditions such as HIV infection, treating oxidative stress in a patient,
XX XX reducing a condition associated with fetal alcohol syndrome, or improving
XX XX learning and/or memory in a subject with e.g. Alzheimer's disease or
XX XX Down's syndrome. The ADNF complex polypeptides are also useful in
XX XX designing a drug treatment regime that can be individually tailored for
XX XX each patient affected by neurodegenerative disorders. The polypeptides
XX XX can also be used for diagnosing or treating Huntington's disease,
XX XX Wilson's disease, Parkinson's disease, AIDS-related dementia or
XX XX Tourette's syndrome. The present sequence represents a peptide that
XX XX captured the survival-promoting activity of ADNF I, and is designated
XX XX ADNF-9 or SAL.
XX XX
XX XX Sequence 9 AA:
XX XX
XX XX Query Match 33.3%; Score 40; DB 6; Length 9;
XX XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX XX
XX XX 41 SALRSIPA 49
XX XX |||||
XX XX 1 SALRSIPA 9
XX XX
XX XX RESULT 8
XX XX ADA07952
XX XX ID ADA07952 standard; peptide; 9 AA.
XX XX
XX XX ADA07952;
XX XX
XX XX 20-NOV-2003 (first entry)
XX XX
XX XX Human activity dependent neuroprotective factor (ADNP) peptide #1.
XX XX
XX XX Human; glaucomatous optic neuropathy;
XX XX KM activity dependent neuroprotective factor; ADNP; ophthalmological.
XX XX
XX XX Homo sapiens.
XX XX
XX XX OS US200316544-A1.
XX XX PN
XX XX PD 04-SEP-2003.
XX XX
XX XX 06-JUN-2002; 2002US-00164432.
XX XX

```

PR 07-SEP-2000; 2000US-0230964P.
PR 02-AUG-2001; 2001US-00921029.
XX
PA (CLAR/) CLARK A F.
PA (SHAD/) SHADE D L.
XX
PI Clark AF, Shade DL;
XX
DR WPI; 2003-720933/68.
XX
PT Treating glaucomatous optic neuropathy by administering a composition
PT comprising a peptide derived from or related to Activity Dependent
PT Neuroprotective Factor (ADNP).
XX
PS Claim 5; Page 2; 13pp; English.
XX
CC The present invention relates to a method for preventing and treating
CC glaucomatous optic neuropathy. The method comprises administering a
CC composition comprising a peptide derived from actively dependent
CC neuroprotective factor (ADNP). The method is useful for treating
CC glaucomatous optic neuropathy. The present sequence represents a peptide
CC from human ADNP.
XX
SQ Sequence 9 AA;
Query Match 33.3%; Score 40; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 SALRSIPA 49
Db 1 SALRSIPA 9
RESULT 9
ADCI6629
ID ADCI6629 standard; peptide; 9 AA.
XX
AC ADCI6629;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human heat shock protein 60 peptide p277 analogue Seq ID7.
XX
KW heat shock protein; Hsp; antigen presenting cell; dendritic cell; T cell;
KW immunomodulatory cytokine; cytokine; chemokine; surface antigen;
KW parasitic disease; inflammatory disease; autoimmune disease;
KW graft rejection; cancer; allergy; Hep60; antiinflammatory;
KW immunosuppressive; antiparasitic; cyostatic; antiallergic; gene therapy;
KW human; p277(442-450, Ser6Ser11).
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003063759-A2.
XX
PD 07-AUG-2003.
XX
PF 30-JAN-2003; 2003WO-IL000078.
XX
PR 31-JAN-2002; 2002US-0352594P.
XX
PA (PEPT-) PEPTOR LTD.
XX
PI Karmon Y, Avron A, Elias D;
XX
DR WPI; 2003-663414/62.
XX
PT Identifying a heat shock protein (Hsp) derived peptide for diagnosing or
PT treating e.g. cancer by comparing the amount of cytokines produced by T
PT cells exposed to antigen presenting cells not previously exposed to the
PT test peptide.
XX

PS Claim 23; SEQ ID NO 7; 47pp; English.
XX
CC This invention relates to a novel heat shock protein (Hsp) derived
CC peptide for use in diagnosis or therapy. Exposure of antigen presenting
CC cells, particularly dendritic cells, to peptides or peptide analogues
CC derived from heat shock proteins subsequently activates T cells to
CC produce immunomodulatory cytokines and will directly influence the
CC cytokines, chemokines and surface antigens produced by the exposed
CC antigen presenting cells. The present invention provides peptides and
CC peptide analogues of heat shock proteins capable of directly interacting
CC with dendritic cells. The peptides of the invention may be useful for the
CC treatment of parasitic, inflammatory or autoimmune disease or graft
CC rejection, cancer or allergy. The preferred peptides of the invention are
CC peptide fragments (p277) or analogues (of p277), derived from heat shock
CC protein Hep60. They may have antiinflammatory, immunosuppressive,
CC antiparasitic, cyostatic or antiallergic activities. The peptide
CC sequences of the invention may also be useful for gene therapy. The
CC present sequence is the amino acid sequence of human heat shock protein
CC (Hsp) 60 peptide fragment p277 analogue p277 (442-450, Ser6Ser11) of the
CC invention.
XX
SQ Sequence 9 AA;
Query Match 33.3%; Score 40; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 SALRSIPA 49
Db 1 SALRSIPA 9
RESULT 10
ADQ76120
ID ADQ76120 standard; peptide; 9 AA.
XX
AC ADQ76120;
XX
DT 07-OCT-2004 (first entry)
XX
DE ADNP I active core site peptide SEQ ID NO:1.
XX
KW activity dependent neurotropic factor; ADNF; ADNF I; active core site;
KW immunosuppressive; nootropic; neuroprotective; antiinflammatory;
KW vasotrophic; muscular; CNS; thymimetic; antithyroid; antirheumatic;
KW antiarthritis; hepatotropic; virucide; dermatological; haemostatic;
KW antidiabetic; antibacterial; neurotropic factor agonist;
KW autoimmune disease; multiple sclerosis; myasthenia gravis;
KW Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;
KW Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;
KW hypothyroiditis; primary biliary cirrhosis;
KW mixed connective tissue disease; chronic active hepatitis;
KW Graves' disease; hyperthyroiditis; scleroderma;
KW chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2004060309-A2.
XX
PD 22-JUL-2004.
XX
PF 30-DEC-2003; 2003WO-US041540.
XX
PR 02-JAN-2003; 2003US-0437650P.
XX
PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Gores I, Offen D, Giladi E, Melamed E, Breneman D;
XX
DR WPI; 2004-543782/52.
XX

PT Preventing or treating autoimmune diseases, such as multiple sclerosis,
PT rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic
PT shock, using an Activity Dependent Neurotrophic Factor (ADNF) polypeptide.
XX
PS Claim 1; SEQ ID NO 1; 39pp; English.
XX
CC The present invention describes a method for preventing or treating an
CC autoimmune disease in a subject. The method comprises administering an
CC activity dependent neurotrophic factor (ADNF) polypeptide, where the ADNF
CC polypeptide is a member selected from the group consisting of: (a) an
CC ADNF I polypeptide comprising an active core site with the amino acid
CC sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide
CC comprising an active core site with the amino acid sequence of SEQ ID
CC NO:2 (ADQ76121); and (c) a mixture of the ADNF I polypeptide of part (a)
CC and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
CC host cells, vectors and antibodies used in the methods are also disclosed
CC in the present invention. ADNF sequences have immunosuppressive,
CC neurotrophic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
CC thyromimetic, antithyroid, antirheumatic, antiarthritic, hepatotropic,
CC virucide, dermatological, haemostatic, antidiabetic and antibacterial
CC activities, and can be used as neurotrophic factor agonists. The methods
CC and compositions of the present invention are useful for the prevention
CC and/or treatment of autoimmune diseases, such as multiple sclerosis,
CC myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,
CC Bence's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
CC disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
CC tissue disease, chronic active hepatitis, Graves'
CC disease/hypothyroiditis, scleroderma, chronic idiopathic
CC thrombocytopenic purpura, diabetic neuropathy and septic shock. The
CC present sequence represents an ADNF I active core site peptide from the
CC present invention.
XX
SQ Sequence 9 AA;
XX
Query Match 33.3%; Score 40; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 SALLRSIPA 49
Db 1 SALLRSIPA 9
XX
RESULT 11
AD873608
ID AD873608 standard; peptide; 9 AA.
XX
AC AD873608;
XX
DT 16-DEC-2004 (first entry)
XX
DE ADNF I active core site.
XX
KW active; core peptide; Activity Dependent Neurotrophic Factor; ADNF;
KW ADNF I; ADNF III; anxiety; depression; lipidilic motility;
KW penetration; activity; panic disorder; obsessive-compulsive disorder;
KW post-traumatic stress disorder; social phobia; social anxiety disorder;
KW specific phobia; generalized anxiety disorder; Major depression;
KW dysthymia; bipolar disorder; NAP-tubulin; binding site; anxiolytic drug;
KW neuroprotection.
XX
OS Homo sapiens.
XX
PN WO2004080957-A2.
XX
PD 23-SEP-2004.
XX
PF 11-MAR-2004; 2004WO-IL000232.
XX
PR 12-MAR-2003; 2003US-0454505P.
XX
PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
XX

PI Gozes I, Alcalay RN, Divinski I, Giladi E;
XX
XX WPI; 2004-668930/65.
DR
XX
XX Treating or preventing anxiety or depression in a subject comprises
PT administering an amount of an Activity Dependent Neurotrophic Factor
PT polypeptide to the subject.
XX
PS Claim 2; SEQ ID NO 1; 46pp; English.
XX
XX This sequence represents the active core peptide derived from Activity
CC Dependent Neurotrophic Factor (ADNF) I. This peptide may be used for
CC treating or preventing anxiety or depression in a subject. This sequence
CC may optionally be extended at either the N- and/or the C-terminals. The
CC ADNF polypeptide of the invention may be encoded by a nucleic acid that
CC is administered to the subject. It also contains a covalently bound
CC lipidilic motility to enhance penetration or activity. The subject suffers
CC from anxiety or depression and the ADNF polypeptide is administered to
CC prevent anxiety or depression. The disease is selected from a panic
CC disorder, obsessive-compulsive disorder, post-traumatic stress disorder,
CC social phobia, social anxiety disorder, specific phobias, generalized
CC anxiety disorder, Major depression, dysthymia, and bipolar disorder. The
CC NAP-tubulin binding site(s) is/are used to identify anxiolytic drugs and
CC drugs that alleviate depression and provide neuroprotection.
XX
SQ Sequence 9 AA;
XX
Query Match 33.3%; Score 40; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 SALLRSIPA 49
Db 1 SALLRSIPA 9
XX
RESULT 12
AAW64690
ID AAW64690 standard; protein; 10 AA.
XX
AC AAW64690;
XX
DT 04-NOV-1998 (first entry)
XX
DE Human ADNF-III antigenic peptide #2.
XX
KW Activity dependent neurotrophic factor III: ADNF-III; ADNF; cell death;
KW activity dependent neuroprotective protein; neurone; excitotoxicity;
KW spinal cord; hippocampus; cerebral cortex; cholinegic; beta-amyloid;
KW N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
KW HIV infection.
XX
OS Synthetic.
XX
PN WO9835042-A2.
XX
PD 13-AUG-1998.
XX
PF 06-FEB-1998; 98WO-US002485.
XX
PR 07-FEB-1997; 97US-0037404P.
XX
PA (USSH) US SEC HEALTH & HUMAN SERVICES.
XX
PI Gozes I, Breneman DE, Baasan M;
XX
DR WPI; 1998-447239/38.
XX
PT Activity dependent neurotrophic factor III polypeptide - useful
PT therapeutically to prevent neuronal cell death associated with e.g. HIV
PT infection, excitotoxicity or Alzheimer's disease.
XX
XX Example 4b; Page 67; 121pp; English.
PS

XX This sequence represents a peptide used in a method which isolates a
 CC novel activity dependent neurotrophic factor III, ADNF-III (also known as
 CC activity dependent neuroprotective protein, ADNP). ADNF III polypeptides
 CC can be used to prevent neuronal cell death, of e.g. the spinal cord,
 CC hippocampal, cerebral cortical or cholinergic neurons associated with
 CC e.g. HIV infection, excitotoxicity induced by N-methyl-D-aspartate
 CC stimulation or beta-amyloid peptide in Alzheimer's disease. The
 CC polypeptides can also be combined with a carrier to alleviate learning
 CC impairment produced by cholinergic blockage in Alzheimer's patients. The
 CC nucleic acids are useful in polypeptide production and to detect ADNF III
 CC polynucleotide in biological samples, while the antibodies are useful
 CC therapeutically and to isolate ADNF III polypeptides
 CC
 XX Sequence 10 AA;
 SQ
 Query Match 33.3%; Score 40; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 41 SALLRSIPA 49
 Db 2 SALLRSIPA 10
 RESULT 13
 AAY71154
 ID AAY71154 standard; peptide; 10 AA.
 AC AAY71154;
 XX
 DT 08-SEP-2000 (first entry)
 DE Peptide CSALLRSIPA used for affinity column chromatography.
 XX
 KM Activity Dependent Neurotrophic Factor III; ADNF; chromosome 20q13.2;
 KM Activity Dependent Neuroprotective Protein; ADNP; neuronal cell death;
 KM autosomal dominant nocturnal frontal-lobe epilepsy; ADNFLE;
 KM neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;
 KM Alzheimer's disease; beta-amyloid peptide; Huntington's disease;
 KM epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;
 KM amyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;
 KM mitochondrial abnormality; Wernicke's encephalopathy; homocysteinuria;
 KM hyperprolinemia; sulphite oxidase disease; Tourette's syndrome; noctropic;
 KM Down's syndrome; drug addiction; developmental retardation; anillipenic;
 KM learning impairment; anticonvulsant; neuroprotective; anti-HIV.
 XX
 OS Unidentified.
 XX
 XX WO200027875-A2.
 XX
 PD 18-MAY-2000.
 XX
 PF 04-NOV-1999; 99WO-US026213.
 XX
 PR 06-NOV-1998; 98US-00187330.
 XX
 XX (USAS) GOVERNMENT US REPRESENT AS.
 PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 XX
 PI Gozes I, Brenneman DE, Baasan M, Zamostiano R;
 DR WPI; 2000-376491/32.
 XX
 DR WPI; 2000-376491/32.
 XX
 PT New nucleic acid encoding an activity dependent neurotrophic factor III
 PT (ADNF III) useful in the treatment of neurological deficiencies and for
 PT preventing neuronal cell death.
 XX
 XX Example; Page 71; 136pp; English.
 PS
 XX The present peptide sequence is used for affinity column chromatography,
 CC for purification of antibodies to Activity Dependent Neurotrophic Factor,
 CC (ADNF), also called an Activity Dependent Neuroprotective Protein (ADNP).

CC The human gene is mapped to chromosome 20q13.2 and is linked to autosomal
 CC dominant nocturnal frontal-lobe epilepsy (ADNFLE) gene. It is expressed
 CC in the astrocytes, brain and also in foetal lung and endocrine tissues.
 CC This sequence has homology to ADNF I and hsp60, heat shock protein and
 CC prn1, a DNA repair protein. The ADNF III polypeptides are useful for the
 CC treatment of neurological deficiencies and for prevention of neuronal
 CC cell death associated with gp120, the envelope protein from HIV; N-methyl
 CC -D-Aspartic acid (excito-toxicity); tetrodotoxin (blockage of electrical
 CC activity); and beta-amyloid peptide, a substance related to neuronal
 CC degeneration in Alzheimer's disease. It is useful for the treatment of
 CC Huntington's disease, AIDS dementia complex, epilepsy, neuropathic pain
 CC syndromes, Parkinson's disease, amyotrophic lateral sclerosis (ALS),
 CC mitochondrial abnormalities, Leber's disease, Wernicke's encephalopathy,
 CC Alzheimer's disease, homocysteinuria, hyperprolinemia, sulphite oxidase
 CC disease, Tourette's syndrome, oxidative stress induced neuronal death,
 CC Down's syndrome, developmental retardation and learning impairments, drug
 CC addiction, tolerance and dependency
 CC
 XX Sequence 10 AA;
 SQ
 Query Match 33.3%; Score 40; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 41 SALLRSIPA 49
 Db 2 SALLRSIPA 10
 RESULT 14
 AAB23487
 ID AAB23487 standard; peptide; 10 AA.
 AC AAB23487;
 XX
 DT 14-MAY-2003 (revised)
 DT 22-JAN-2001 (first entry)
 DE
 XX
 KM Activity dependent neurotrophic factor I peptide #19.
 KM
 KM Activity dependent neurotrophic factor; ADNF; FAS;
 KM foetal alcohol syndrome; gene therapy; neurological deficiency;
 KM neuronal cell death.
 XX
 OS Unidentified.
 XX
 XX WO200053217-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 10-MAR-2000; 2000WO-US006364.
 XX
 PR 12-MAR-1999; 99US-00267511.
 XX
 XX (UYRA-) UNIV RAMOT.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Brenneman DE, Spong CY, Gozes I, Baasan M, Zamostiano R;
 DR WPI; 2000-601940/57.
 XX
 DR WPI; 2000-601940/57.
 XX
 PT Treating condition associated with fetal alcohol syndrome in a subject
 PT exposed to alcohol in utero or reducing neuronal death, involves
 PT administering activity dependent neurotrophic factors I and/or III.
 XX
 XX Claim 6; Page 4; 65pp; English.
 PS
 XX The present invention relates to the treatment of a condition associated
 CC with foetal alcohol syndrome (FAS), involving administering an activity
 CC dependent neurotrophic factor (ADNF). ADNFs of the present invention may
 CC also be used to treat neurological deficiencies and prevent neuronal cell
 CC death. The present sequence is an ADNF peptide. (Updated on 14-MAY-2003
 CC to correct PS field.)

XX
SQ Sequence 10 AA;

Query Match 33.3%; Score 40; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49
|||
Db 2 SALLRSIPA 10

Db |||
2 SALLRSIPA 10

Search completed: February 23, 2005, 19:30:07
Job time : 121.175 secs

RESULT 15

AAB72321
ID AAB72321 standard; peptide; 10 AA.

XX AAB72321;

DT 16-MAY-2001 (first entry)

DE Activity dependent neurotrophic factor I (ADNF I) peptide SEQ ID 19.

XX Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;
KM neuronal cell death; Alzheimer's disease; oxidative stress; VIP;
KM vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.

XX Synthetic.

XX WO200112654-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US022861.

XX 18-AUG-1999; 99US-0149956P.

XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Breneman DE, Gozes I, Spong CY, Pinhasov A, Giladi E;

XX WPI; 2001-202855/20.

PT Novel Activity Dependent Neurotrophic Factor I useful for treating
PT oxidative stress, reducing neuronal cell death and treating a condition
PT associated with fetal alcohol syndrome.

PS Claim 7; Page 56; 88pp; English.

XX This invention relates to an activity dependent neurotrophic factor I
CC (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72321 represent
CC ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent
CC ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical
CC composition containing either ADNF I or ADNF III are useful for reducing
CC neuronal cell death, e.g. death of spinal cord neurons, hippocampal
CC neurons, cerebral cortical neurons and cholinergic neurons, in a patient
CC infected with a virus, e.g. human immunodeficiency virus (HIV). The
CC neuronal cell death is associated with excitotoxicity induced by N-
CC methyl-D-aspartate (NMDA) stimulation, which is induced by beta-amyloid
CC peptide in an Alzheimer's disease patient, or induced by cholinergic
CC blockade. ADNF I, ADNF III and the pharmaceutical composition are also
CC useful for treating oxidative stress in a patient, for reducing a
CC condition, such as decreased body weight, decreased brain weight,
CC decreased level of vasoactive intestinal peptide (VIP) mRNA, and foetal
CC death, associated with foetal alcohol syndrome

XX SQ Sequence 10 AA;

Query Match 33.3%; Score 40; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 SALLRSIPA 49